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Sequence 9, Appli
Sequence 15, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 5741, Ap
Sequence 12702, A
Sequence 12702, A
Sequence 12812, A
Sequence 843, Appl
Sequence 843, Appl
                                                                                                                                                                       Sequence 20, Appl Sequence 519, Ap Sequence 519, Ap Sequence 12263, Ap Sequence 12, Appl Sequence 32, Appl Sequence 64, Appl Sequence 61, Appl Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl Sequence 263, Appl Sequence 263, Appl
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TITLE OF INVENTION: THERAPEUTIC COMPOUNDS FOR OVARIAN CANCER
FILE REPERENCE: 6812689100
CURRENT APPLICATION NUMBER: 09/09/670,089B
CURRENT FILING DATE: 2001-05-30
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1296, Application US/09925300
Patent No. US20020151681A1
BAPLICANT: Craig Rosen,
APPLICANT: Steve Ruben
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REPERENCE: PA101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 55; DB 12;
100.0%; Pred. No. 6.1e+05;
live 0; Mismatches 0;
US-09-895-072-15
US-09-986-552-15
US-10-024-197-9
US-10-024-197-9
US-10-023-889-9
US-10-023-889-9
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US-09-815-242-12563
US-09-815-242-12563
US-09-815-242-5419
US-10-10-10-121-18
US-10-10-10-121-18
US-10-045-792-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 13, Application US/09870089B; Publication No. US20030175252A1; GENERAL INFORMATION:
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   Query Match
Best Local Similarity 100.
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US-09-925-300-1296
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  TYPE: PRT
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Sequence 252, Appl
Sequence 8, Appli
Sequence 10, Appl
Sequence 47039, A
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Sequence 89, Appl
Sequence 14, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 13, App.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution
                                                                                     2003, 14:18:11; Search time 22.1667 Seconds (without alignments) 75.512 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

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18: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
              GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-925-300-1296 ·· US-09-925-300-1296 ·· US-09-882-27-252

US-09-882-27-252

US-09-116-788A-10

US-09-864-761-47039

US-09-864-761-47039

US-09-815-242-10094

US-09-120-801-89

US-09-120-801-89

US-09-120-801-89

US-10-120-801-89

US-10-128-073-2

US-10-258-073-2

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Maximum Match 100%
Listing first 45 summaries
                                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Match Length
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64.33
64.33
64.33
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64.36
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us-09-870-089b-13.rapb

Page 2

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APPLICANT: Kleanthous, Harold
APPLICANT: Al-Garawi, Amal
APPLICANT: Miler, Charles
APPLICANT: Miler, Charles
APPLICANT: Miler, Charles
APPLICANT: Tomb, Jean-Francois
APPLICANT: Ocomen, Fawmond by
TITLE OF INVENTION: Encoding No. US20030158396Alel Helicobacter Polypeptides in the FITTLE OF INVENTION: Genome
TITLE OF INVENTION: Genome
FILE REFERENCE: 06132/047002
CURRENT APPLICATION NUMBER: US/09/082,227
CURRENT APPLICATION NUMBER: US/09/025
PRIOR FILING DATE: 1997-07-29
PRIOR FILING DATE: 1997-07-29
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Pred. No. 0.074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FREREAL INFORMATION:

APPLICANT: McDonald, Thomas L.

APPLICANT: McDonald, Thomas L.

APPLICANT: Weber, Annika

ITILE OF INVENTION: Genomic Mammary Amyloid A Sequence

FILE REFERENCE: P04557US1

CURRENT APPLICATION NUMBER: US/10/116,788A

CURRENT FILING DATE: 1999-10-22

PRIOR APPLICATION NUMBER: 09/425,679

PRIOR APPLICATION NUMBER: 60/218,482

PRIOR APPLICATION NUMBER: 60/218,482

PRIOR APPLICATION NUMBER: 60/218,482

PRIOR APPLICATION NUMBER: 60/218,482

PRIOR APPLICATION NUMBER: 50/0-07-14

PRIOR APPLICATION NUMBER: 2000-07-14

PRIOR FILING DATE: 2000-07-14

NUMBER OF SEQ ID NOS: 34

SOFTWARE: Patentin version 3.1
                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 638
SOFTWARE FeatSEQ for Windows Version 4.0
SEQ ID NO 252
LENGTH: 348
                                                                                                                                                                                                                                                              ; Sequence 252, Application US/09882227; Publication No. US20030158396A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/10116788A; Publication No. US20030170840A1; GENERAL INFORMATION:
                       Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Helicobacter pylori
                                             9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Equus caballus
                                                                                                                                       42 KHFKPHGFS 50
                                                                                            1 KHFKPHGFS 9
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                                                  Matches
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TITLE OF INVENTION: Differentially Regulated Prostate Cancer Genes
FILE REFERENCE: 9U 204 205 R1
CURRENT APPLICATION NUMBER: US/10/341,434
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US 60/348,164
PRIOR FILING DATE: 2002-01-15
PRIOR FILING DATE: 2002-01-15
PRIOR FILING DATE: 2002-01-15
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                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 55; DB 10; Length 286; Best Local Similarity 100.0%; Pred. No. 0.06; Matches 9; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Charles A. Nicolette
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS FOR OVARIAN CANCER
FILE REFERENCE: 68126881209900
CURRENT APPLICATION NUMBER: US/09/870,089B
CURRENT FILING DATE: 2001-05-30
NUMBER OF SEQ ID NOS: 14
SOFTMARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
                  CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR PILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: Patentin Ver. 2.0
SENGTH: 286
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; Sequence 67, Application US/10341434
; Publication No. US20030215835A1
; GENERAL INFORMATION:
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SOFTWARE: Patentin version 3.1
SEQ ID NO 67
LENGTH: 351
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ORGANISM: Homo sapiens
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Matches 9; Conserve
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IS-09-870-089B-2
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US-09-870-089B-2
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EXPRESSED IN LUNG, SIGNAL = 0.52

EXPRESSED IN ADULT LIVER, SIGNAL = 0.58

EXPRESSED IN BONE MARROW, SIGNAL = 1.2

EST HUMAN HIT: AL553866.1, EVALUE 5.00e-25

SWISSPROT HIT: Q16515, EVALUE 2.00e-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Oblean, Kari L.
APPLICANT: Oblean, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Tradick, John D.
APPLICANT: Tradick, John D.
APPLICANT: Tradick, John D.
APPLICANT: Yanamoto, Robert T.
APPLICANT: Yanamoto, Robert T.
APPLICANT: Xu, H. Howard
ITILE OF INVENTION: Identification of Essential Genes.in
TITLE OF INVENTION: Prokaryotes
ITILE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: 00/09/815,242
PRIOR APPLICATION NUMBER: 00/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PLLING DATE: 2000-11-27
PRIOR PLLING DATE: 2000-11-27
PRIOR PLLING DATE: 2000-11-27
PRIOR PLLING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 35; DB 9; Length 96;
Pred. No. 66;
1; Mismatches 2; Indels
                                                 FRIOR PILICALION NUMBER: PCT/USOL/USORB
FRIOR PELICATION NUMBER: PCT/USOL/USORB
FRIOR APPLICATION NUMBER: PCT/USOL/00663
FRIOR APPLICATION NUMBER: PCT/USOL/00662
FRIOR APPLICATION NUMBER: PCT/USOL/00662
FRIOR APPLICATION NUMBER: PCT/USOL/00661
FRIOR PILING DATE: 2001-01-30
FRIOR PILING DATE: 2001-01-30
FRIOR PILING DATE: 2001-01-30
FRIOR PILING DATE: 2000-00-21
FRIOR APPLICATION NUMBER: US 60/234,687
FRIOR APPLICATION NUMBER: US 09/608,408
FRIOR PILING DATE: 2000-06-30
FRIOR PILING DATE: 2000-06-30
FRIOR PILING DATE: 2000-06-30
FRIOR PILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SEQ ID NO 47039
LENGTH: 96
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Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h 63.6%;
Similarity 66.7%;
6; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50 KHYKPKQFS 58
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OTHER INFORMATION: M.
OTHER INFORMATION: E.
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Matches 6; Conserv
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APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES US OF TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES US OF TITLE OF INVENTION NUMBER: US 00/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/23,366
PRIOR FILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: PCT/US01/00666
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US-10-116-788A-10
Sequence 10, Application US/10116788A
Sequence 10, Application US/10116788A
Sequence 10, Application US/10116788A
Sequence 10, Application Sequence 10, Application No. US20030170840A1
Sequence 10, Application Sequence 11 TILE OF INVENTION: Genomic Mammary Amyloid A Sequence 11 TILE OF INVENTION: Genomic Mammary Amyloid A Sequence 11 TILE OF INVENTION: ED46557US1
CURRENT APPLICATION NUMBER: US/10/116,788A
CURRENT APPLICATION NUMBER: 09/425,679
PRIOR APLICATION NUMBER: 60/218,482
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 60/218,611
PRIOR FILING DATE: 2000-07-17
SEQUENCE FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
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APPLICATION NUMBER: PCT/US01/00667
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APPLICATION NUMBER: PCT/US01/00664
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APPLICATION NUMBER: PCT/US01/00665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 47039, Application US/09864761
Patent No. US20020048763A1
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Matches 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Equus caballus
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100 HFRPHG 105
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HFRPHG 12
HFKPHG 7
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US-09-983-204-14
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            APPLICANT:
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                                                                                                                                                                                                                                              ery Match 63.6%; Score 35; DB 9; Length 244; st Local Similarity 71.4%; Pred. No. 1.7e+02; tches 5; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yumanoto, Robert T.
APPLICANT: Xu, H. Howard
ITTLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILLE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: US/09/815,242
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-21
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-3
PRIOR PILING DATE: 2000-05-3
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-3
PRIOR FILING DATE: 2000-10-3
PRIOR PILING DATE: 2000-10-3
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-12-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: PASLESEQ FOR WINDOWS VERSION 4.0
SED ID NO 13891
IOR FILING DATE: 2001-02-16
MBER OF SEQ ID NOS: 14110
)FTWARE: FASESEQ for Windows Version 4.0
)ID NO 10094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ULT 10
09-815-242-13891
equence 13891, Application US/09815242
atent No. US20020061569A1
ENERAL INFORMATION:
APPLICANT: Hacelbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 89, Application US/10120801
; Publication No. US/0030203843A1
; GENERAL INFORMATION
; APPLICANT: Pena, Carol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT; ORGANISM: Salmonella typhi
US-09-815-242-13891
                                                                                                                                                CYPE: PRT
ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101 RHVKPHG 107
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US-10-120-801-89
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0; Gaps
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ITILE OF INVENTION: Protectins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-340
FILE REFERENCE: 21402-340
CURRENT APPLICATION NUMBER: US/10/120,801
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: 60/28608
PRIOR FILING DATE: 2001-04-23
PRIOR FILING DATE: 2001-04-24
PRIOR FILING DATE: 2001-04-25
PRIOR FILING DATE: 2001-05-03
PRIOR FILING DATE: 2001-05-04
PRIOR FILING DATE: 2001-05-05
PRIOR FILING DATE: 2001-09-14
PRIOR FILING DATE: 2001-09-14
PRIOR FILING DATE: 2001-09-14
PRIOR FILING DATE: 2001-09-14
PRIOR FILING DATE: 201-04-20
NUMBER OF SQL ID NOS: 155
SOFFMARE: PARENTEN VONES: 155
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APPLICANT: RENARD, STEPHANE
APPLICANT: GRAHAM, DAVID
APPLICANT: GRAHAM, DAVID
TILE OF INVENTION: SODIUM CHANNEL RECEPTOR
FILE REFRENCE: 0.7586.0010
CURRENT APPLICATION NUMBER: 0.9/424,666
PRIOR APPLICATION NUMBER: 0.9/424,666
PRIOR APPLICATION NUMBER: 0.9/424,666
PRIOR APPLICATION NUMBER: 9740196.7
PRIOR APPLICATION NUMBER: 97401196.7
PRIOR PILING DATE: 1998-05-15
PRIOR PILING DATE: 1998-05-15
PRIOR FILING DATE: 1997-05-30
NUMBER: 0.50FWARE: PatentIn Ver: 2.0
SEQ ID NO 14
LENGTH: 512
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; Patent No. US20020173000A1
                   Shimkets, Richard
Padigaru, Muralidhara
Kekuda, Ramesh
Spytek, Kimberly
                                                                                                                                                                                                                                                                                 Smithson, Glennda
Gunther, Erik
Komuves, Laszlo
                                                                                                                                   Mehraban, Fuad
Topper, James N.
Malyankar, Uriel
Wasserman, Scott
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Guo, Xiaojia
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ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 HFKPHGFS 9
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Best Local Similarity
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US-10-120-801-89
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144 KHYKPKQFS 152
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Publication No. US20030219858A1

GENERAL INFORMATION:

APPLICANT: McGill University

APPLICANT: Sequela, Philippe

TITLE OF INVENTION: A NOVEL HETERCOMULTIMERIC ION CHANNEL RECEPTOR AND USES

TITLE OF INVENTION: THEREOF

FILE REFERENCE: 0103.001-WO-US

CURRENT APPLICATION NUMBER: US/10/258,073

CURRENT PAPLICATION NUMBER: DC/100-04

PRIOR APPLICATION NUMBER: PC/7/CA01/00561

PRIOR FILING DATE: 2000-04-20

NUMBER OF SEQ ID NOS: 28

SOFTWARE: Patentin Ver: 2.1

SEQ ID NO 6

LENGTH: 512
                                                                                                                                                                                                                                                             RESULT 13
US-10-258-073-2
; Sequence 2, Application US/10258073
; Publication No. US20030219858A1
; Publication No. US20030219858A1
; GENERAL INFORMATION:
; APPLICANT: McGill University
; APPLICANT: Babinski, Kazimierz
APPLICANT: Sequela, Philippe
; TITLE OF INVENTION: A NOVEL HETEROMULTIMERIC ION CHANNEL RECEPTOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 0103.001-W0-US
; CURRENT APPLICATION NUMBER: US/10/258,073
; CURRENT APPLICATION NUMBER: PCT/CA01/00561
; PRIOR PILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver: 2.1
; SEQ ID NO 2
: LENGTH: 512
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                                                              63.6%; Score 35; DB 10; Length 512; 66.7%; Pred. No. 3.7e+02; Live 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 66.7%; Pred. No. 3.7e+02;
Matches 6; Conservative 1; Mismatches 2; Indels
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                                                                 Query Match 63.6
Best Local Similarity 66.7
Matches 6; Conservative
; OTHER INFORMATION: MDEG
US-09-983-204-14
                                                                                                                                                                                          144 KHYKPKQFS 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: HUMAN ASIC2A
US-10-258-073-2
                                                                                                                                                            1 KHFKPHGFS 9
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; ORGANISM: RAT ASIC2A
US-10-258-073-6
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US-10-258-073-6
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RESULT 15
US-10-032-565-7813
US-10-032-565-7813
Sequence 7813, Application UG/10032585
Publication No. US20030180953A1
GENERAL INFORMATION:
APPLICANT Terry. Roemer D.
APPLICANT Terry. Roemer D.
APPLICANT: Howard, Bussey
TILE REPRENCE: 10182-005-999
CURRENT FILING DATE: US/10/032,585
CURRENT FILING DATE: 2001-12-20
NUMBER OF EXQ ID NOS: 8000
SEQ ID NO 7813
CURRENT PLING DATE: PatentIn version 3.1
SEQ ID NO 7813
CURRENT FILING
SEQ ID NOS: 8000
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7813
CURRENT FILING
SEC ID NOS: 8000
SERVICE REPRENCE: 10182-005-999
CURRENT FILING
SEQ ID NOS: 8000
SERVICE REPRENCE: 10182-005-999
CURRENT FILING
SEQ ID NOS: 8000
SERVICE REPRENCE: 10182-005-999
CURRENT FILING
SEQ ID NOS: 8000
SERVICE REPRENCE: 10182-005-999
CURRENT FILING
SEQ ID NOS: 8000
SERVICE REPRENCE: 10182-005-999
CURRENT MATCH OF SEQ ID NOS: 8000
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SERVICE REPRENCE: 10182-005-999
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43.289 Million cell updates/sec
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| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDSI/gcgdata/geneseq-geneseqp-embl/AA1982.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseqfgeneseqp-embl/AA1989.DAT:*
| SIDSI/gcgdata/geneseqfgeneseqp-embl/AA1989.DAT:*
| SIDSI/gcgdata/geneseqfgeneseqp-embl/AA1980.DAT:*
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| SIDSI/gcgdata/geneseqfgeneseqp-embl/AA1990.DAT:*
| SIDSI/gcgdata/geneseqfgeneseqpeembl/AA2001.DAT:*
                                                                                                                                                                                                                                                                                      December 16, 2003, 14:06:05; Search time 33 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1107863
                               GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	Description	Human cancer antic	Novel human diagno	Human secreted pro-	Novel human diagno	Human prostate can	Human cancer antio	Novel human diagno	Novel human diagno	Mouse ischaemic co
	ID	AAU74686	ABG17297	AAG00153	ABG17298	AAB56718	AAU74680	ABG17300	ABG17299	ABB57035
	DB	23	22	21	22	21	23	22	22	23
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	Score	55	55	55	55	55	55	55	55	49
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H. pylori GHPO 632 AARS645	ALIGNMENTS AA. B-2 natural immunogenic ligand. CREB-2; vaccine; cytostatic; apy; MHC; major histocompatibility complex; r; ovarian cancer.
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24	Peptidd t entry) en ATF4, en ATF4, gene trapy; carapy;
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N-PSDB; AAS81484.
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                                                                  biodiversity
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                                                           The invention relates to compounds comprising an immunogenic ligand whose sequence is based in part on residues 42-50 of human cancer antigen ATF4/CREB-2 (not defined) and the polynuclectides encoding them. Also included are an antibody that specifically recognises and binds the compound, a method for inducing an immune response in a subject by delivering the compound, a method of immunotherapy comprising administering to a subject the antibody, an immune effector cell that has been raised in vitro or in vivo in the presence and at the expense of an entiped presenting cell that presents the immunogenic compound in the context of an MHC (major histocompatibility complex) molecule and a method of adoptive immunotherapy comprising administering the immune effector cell. The compounds are useful for modulating an immune response to the synthetic and naturally occurring compounds. The compounds are useful for reating cancer, particularly ovacines. The compounds are useful for treating cancer, particularly ovacines. The compounds are useful for reating cancer, particularly ovacines. The compounds are useful for immunotherapy when administered to a subject. The peptides, polypeptides and polynucleotides are useful in diagnostic methods, for the detection and purification of antibodies, or as immunogens for the production of antibodies. The sequence represents a human cancer antigen ATF4/CREB-2 based immunogenic sequence represents.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
modulating an immune response, particularly for treating ovarian
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food supplement; medical imaging; diagnostic; genetic disorder.
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100.0%; Pred. No. 9.3e+05;
tive 0; Mismatches 0;
             cancer, and as components of anticancer vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human diagnostic protein #17288.
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                                       Claim 6; Page 56; 68pp; English.
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23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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ABG17297
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (FGR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding attners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical insolates involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in disponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and anino acid sequences. ABG00010-ABG30377 represent novel human and diagnostic amino acid sequences of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid that is a 5' expressed sequence tag (5' EST) for
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                                                                                                                                                                                                     Claim 20; SEQ ID No 47656; 103pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38 KHFKPHGFS 46
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                                                                                    The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
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                   diagnostic, forensic, gene therapy and chromosome mapping procedures
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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 correspond to 5'ESTs and
                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 55; DB 21; Length 99; 100.0%; Pred. No. 0.011; ive 0; Mismatches 0; Indels
                                                       Claim 13; SEQ ID 4234; 71pp + CD-ROM; English
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genomic DNAs that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human diagnostic protein #17289.
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23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                     Sequence
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for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; prostate cancer; prostate cancer antigen; detection; diagnosis; neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynaccological; antibacterial; gene therapy; neural; immune; reproductive; renal; gastrointestinal; pulmonary; cardiovascular; proliferative disorder; wound; infectious disease.
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                                                                                                                                                                                                                                                                 te: The sequence data for this patent did not appear in the printed ecification, but was obtained in electronic format directly from WIPO ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human prostate cancer antigen protein sequence SEQ ID NO:1296.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB56718 standard; Protein; 286 AA.
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                                                                                                                                                                                                                                                                                                                                                121 AA;
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                                                                                                                                                                                                                                                                                  specification,
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 nephrotropic, antiinfective, gynaecological and antibacterial activities,
               and can be used in gene therapy. The prostate cancer antigen polynucleotides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; cancer antigen; ATF4; CREB-2; vaccine; cytostatic; immunogenic ligand; gene therapy; MHC; major histocompatibility complex; adoptive immunotherapy; cancer; ovarian cancer.
                                                                   or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and prolliferative disorders, wounds, and infectious diseases. AAP16506 to AAF16514 to AAB57303 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New therapeutic compounds comprising immunogenic ligands, useful for modulating an immune response, particularly for treating ovarian cancer, and as components of anticancer vaccines
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20-DEC-2000; 2000US-257007P.
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N-PSDB; AAS20119.
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                                                                                                                                                                     invention.
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especially useful in gene therapy or as components of anti-cancer vaccines. The compounds are useful for treating cancer, particularly ovarian cancer. The compounds are also useful for generating antibodies that specifically recognise and bind to these molecules. These antibodies are further useful for immunotherapy when administered to a subject. The peptides, polypeptides and polymucleotides are useful in diagnostic methods, for the detection and purification of antibodies, or as immunogens for the production of antibodies. The present sequence represents human cancer antigen AT44(CREB-2 upon which the immunogenic ligands of the invention are based.
                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; chromosome mapping; gene mapping; gene therapy, forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human diagnostic protein #17291.
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23-AUG-2000; 2000US-0649167.
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diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                    Gaps
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and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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nes 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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DB 23; Length 346;

89.1%; Score 49;

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N-PSDB; AAS88490
                                                                   WO200175067-A2
                                                  Homo sapiens
                                                                                    11-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAR-2003
06-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR55694;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Matches
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AAR55694
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ·:
                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents a Helicobacter pylori GHPO protein of the invention. The polypepitides can be used for preventing or treating Helicobacter infections, and gastroducdenal diseases associated with these infections, including acute, chronic, and arrophic gastritis, and peptic ulcer diseases, e.g. gastric and duodenal ulcers. They can also be used for the production of antibodies. The products can also be used for detection and diagnosis
                                                                                                                                                   GHPO protein, Helicobacter infection, gastroduodenal disease, gastritis, peptic ulcer disease.
                                                                                                                                                                                                                                                                                                                                                       New isolated Helicobacter polynucleotides - used to develop products for the diagnosis, prevention and treatment of Helicobacter infections and gastrointestinal diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
        Gaps
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0
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ب
        Indels
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                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC.
(INWR ) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
Pred. No. 0.55;
        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                         Claim 8; Page 1444-1446; 2054pp; English.
                                                                                                                                                                                                                                                                                                             Al-Garawi A, Kleanthous H, Miller C,
                                                                                   AAW98693 standard; Protein; 348 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABG24303 standard; Protein; 643 AA.
                                                                                                                                                                                                                                                 97US-0902615.
97US-0833457.
97US-0881227.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78.2%;
88.98;
                                                                                                                                                                                                                                  98WO-US06371.
                                                                                                                                     H. pylori GHPO 632 protein
                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 87.5
nes 7; Conservative
        8; Conservative
                                     39 KHLKPHGFS 47
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N-PSDB; AAX14412.
                                                                                                                                                                               Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 HFKPHGFS 9
                        1 KHFKPHGFS
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             348 AA;
                                                                                                                                                                                                WO9843478-A1
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                                                                                                                    31-MAR-1999
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                                                                                                    AAW98693;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
                                                                  RESULT 10
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags cor identifying expressed genea. (I) is useful in gene therapy techniques correstore normal activity of (II) or to treat disease states involving to restore normal activity of (II) or to treat disease states involving correct or identifying antibodies against it, detecting or quantifating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding artners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical consolidation of sites expressing (II). (I) and (II) are useful in medical sources involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in disgnostics, forenaics, gene mapping, identification of mutations are responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and and to produce other types of data and products dependent on DNA and and cands sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO CC at fip.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated polynuclectide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                   Human, chromosome mapping; gene mapping; gene therapy, forensic; food supplement, medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; SEQ ID No 54662; 103pp; English.
Novel human diagnostic protein #24294.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR55694 standard; Protein; 2391 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (updated)
(first entry)
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les 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 HFKPHGQS 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 HFKPHGFS 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          643 AA;
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The present sequence is encoded by a testis 5' RACE clone type 1, created to characterise the 5' end of the human cancer cachectic factor (CCF) open reading frame. The coding region of CCF has extensive homology to a 20 amino acid sequence obtained from the peptide core of a mouse tumour derived proteoglycan with cachectic effects. CCF, a 24 kD protein factor, induces weight loss, and can be used with a substance capable of reducing appetite or inducing satiety. CCF can alternatively be campaintered with a substance capable of increasing the ratio of lean to fact body mass. CCF is useful for treating conditions or disorders arising from obesity or for inducing weight loss. CCF is used to prevent or treat non-insulin dependent diabetes (NIDDM) or Syndrome X. Anti-CCF antibodies can be used for direct application to cancer patients in order to reduce weight loss and tumour growth. The antibodies can used to diagnose cancer by detecting the presence of p24CCF in urine or serum of potential cancer patients. Antisense CCF gene constructs are useful for the prevention of unwanted endogenous synthesis or activity of CCF, e.g. in potential cancer patients, thus preventing weight loss (tissue degeneration). Labelled CCF or preventing to identify CCF receptors which are then useful for detection of CCF24 kD
                                                                             Human, cancer cachectic factor, p24K-inc, weight loss, treatment, mouse tumour derived proteoglycan, cachectic effect, prevention, non-insulin dependent diabetes, NIDDM; syndrome X; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding a cancer cachectic factor - used to prevent or treat non-insulin dependent diabetes or Syndrome {\sf X}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 40; DB 19; Length 119;
Pred. No. 8;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           Vissing H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster polypeptide SEQ ID NO 9309.
                                       Protein encoded by testis 5' RACE clone type 1.
                                                                                                                                                                                                                                                                                                                                                                                                           Rasmussen PB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB60839 standard; Protein; 1369 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 36; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                         Clausen J, Din N, Farrah TM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72.7%;
77.8%;
                                                                                                                                                                                                                                                                                     97WO-DK00377.
                                                                                                                                                                                                                                                                                                                             96DK-0000968
  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAR-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-207329/18
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAV23110
                                                                                                                                                                                                                                                                                                                         09-SEP-1996;
                                                                                                                                                                                                     WO9811136-A1
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  05-AUG-1998
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ABB60839
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The cDNA sequence encoding the carbamoyl-phosphate-transferase II (CPSII) of Plasmodium falciparum was determined. The cDNA encodes a protein that includes 2 insert sequences not found in other CPSII proteins. The first separates the putative structural subdomain and the glutaminase subdomain of the glutamine-amidotransferase subunit coff CPSII, while the second separates 2 ATP binding subdomains of the CPSII subunit, CPSa and CPSD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid encoding carbamoyl phosphate synthetase II - isolated from Plasmodium falciparum, used to develop prods. for the treatment of malaria.
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                                                                                                                                                                                                                                                                                                                                            /note= "carbamoyl-phosphate-synthase domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 2391;
                                                                                                                                                                              'note= "glutamine-amidotransferase domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                     Carbamoyl-phosphate-synthetase II; CPSII; psCPSII gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note= "ATP binding subdomain CPSb"
                                                                                                                                                                                                                                                                                                                                                                         /note= "ATP binding subdomain CPSa
1255..1857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 41; DB 15;
Pred. No. 1.4e+02;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                    "glutaminase subdomain"
                                                                                                                                                                                                                      'note= "structural subdomain"
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                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "insert sequence"
1858..2391
                                                                                                                                                                                                                                                                "insert sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stewart TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 6-16; 31pp; English.
                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW56455 standard; Protein; 119 AA.
Carbamoyl-phosphate-synthetase II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74.5%;
77.8%;
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92AU-0006380.
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                                                                                                                                                                                                                                                                                                                                                             1254
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Best Local Similarity 77.0
Local 7; Conservative
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|168 KYFKKHGFS 1176
                                                                                                                                                                                                                                                                /note=
                                                                                                                                                                                                                                                                                                    /note=
                                                                                              Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UNIX ) UNISEARCH LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-DEC-1993;
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AAW56455

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McDonald TL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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100.0%; Pred. No. 2.7e+02;
tive 0; Mismatches 0; Indels
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid
genes from Drosophila and
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                                                Drosophila melanogaster.
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N-PSDB; ABL04942.
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  pharmaceutical.
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The patent discloses novel colostrum-associated Serum Amyloid A (SAA) from mammals. SAAs are small apolipoproteins that accumulate and associate rapidly with high-density lipoprotein 3 (HDL3) during the acute phase of inflammatory response. They are characterised by the TFLK motif in the N-terminal region which has the ability to stimulate mucin 3 (MUC3) production. Colostrum associated SAAs are used to prevent or treat infectious diseases associated with enteric pathogens (particularly Escherichia coli) such as traveller's diarrhoea, infant diarrhoea, necrotising enterocolitis (MEC), urinary tract infections, and infectious diarrhoea in herd animals. They are used to prevent dysentery and other infectious diseases particularly much military.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; Page 20; 81pp; English
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83.3%;
22-OCT-1999; 99US-0425679.
14-JUL-2000; 2000US-0218482.
17-JUL-2000; 2000US-0218611.
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                                                                                                                                    (UYNE-) UNIV NEBRASKA
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Matches 5, Conserv
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Scoring table:

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                                                                                                   AAG82248
ABP40155
ABB11608
ABP73980
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ABP81751
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AAO03783
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 31-MAY-2000; 2000US-209388P.
20-DEC-2000; 2000US-257007P.
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| SIDS1/gcgdata/geneseq/geneseqp_embl/AA1980.DAT:*
| SIDS1/gcgdata/geneseqf_embl/AA1981.DAT:*
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            GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                              seq length: 0
seq length: 200000000
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                                                                                                                 December 16,
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528
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Score

Result No.

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The invention relates to compounds comprising an immunogenic ligand whose sequence is based in part on residues 42-50 of human cancer antigen ATF4(FREB-2 (fout defined) and the polymuclecides encoding them. Also included are an antibody that specifically recognises and binds the compound, a method for inducing an immune response in a subject by delivering the compound, a method of immunotherapy comprising deministering to a subject the antibody, an immune effector cell that has been raised in vitro or in vivo in the presence and at the expense of antigen presenting cell that presents the immunogenic compound in the context of an MHC (major histocompatibility complex) molecule and a method of adoptive immunotherapy comprising administering the immune effector cell. The compounds are useful for modulating an immune response to the synthetic and naturally occurring compounds. The compounds are useful for treating cancer, particularly vaccines. The compounds are useful for treating cancer, particularly covarian cancer. The compounds are also useful for generating antibodies that specifically useful for immunotherapy when administered to a subject. The peptides, for the detection and purification of antibodies, or as immunogen for the percent and purification of antibodies. The percent in the production of antibodies. The present cancer antigen ATF4/CRB-2 based immunogenic
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New therapeutic compounds comprising immunogenic ligands, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    but have not been cross-referenced or CDS features put in due to the
                                  modulating an immune response, particularly for treating ovarian cancer, and as components of anticancer vaccines
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 50; DB 23; Length 9; 100.0%; Pred. No. 9.38+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note: Immunogenic ligands AAU74681-AAU74686 are stated to encoded by the degenerate DNA sequences AAS20120-AAS20125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       degeneracy of the DNA sequences.
                                                                                                                                            Claim 5; Page 56; 68pp; English.
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Best Local Similarity
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AAU74682
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The invention relates to compounds comprising an immunogenic ligand whose sequence is based in part on residues 42-50 of human cancer antigan ATP4/CRBB-2 (not defined) and the polymucleotides encoding them. Also included are an antibody that specifically recognises and binds the compound, a method for inducing an immune response in a subject by delivering the compound, an ethod of immunotherapy comprising to a subject the antibody, an immune effector cell that has been raised in vitro or in vivo in the presence and at the expense of an antigen presenting cell that presents the immunogenic compound in the context of an MHC (major histocompatibility complex) molecule and a method of adoptive immunotherapy comprising administering the immune response effector cell. The compounds are useful for modulating an immune response to the synthetic and naturally occurring compounds. The compounds are especially useful in gene therapy or as components of anti-cancer specials.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ovarian cancer. The compounds are also useful for generating antibodies that specifically recognise and bind to these molacules. These antibodies are further useful for immunotherapy when administered to a subject. The peptides, polypeptides and polynucleotides are useful in diagnostic methods, for the detection and purification of antibodies, or as immunogens for the production of antibodies. The present sequence represents a human cancer antigen ATF4/CREB-2 based immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Note: Immunogenic ligands AAU74681-AAU74686 are stated to be encoded by the degenerate DNA sequences AAS20120-AAS20125 respectively but have not been cross-referenced or CDS features put in due to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       identification; cytostatic; cardioactive; neuroprotective; vulnerary; immunomodulatory; muscular; gynaecological; gastrointestinal; nephrotropic; antiinfective; antibacterial; gene therapy; wound; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; renal disorder; infectious disease; cardiovascular disorder.
                                                                                 New therapeutic compounds comprising immunogenic ligands, useful for modulating an immune response, particularly for treating ovarian cancer, and as components of anticancer vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 41; DB 23; Length 9; Pred. No. 9.3e+05; 1; Mismatches 1; Indels
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                                                                                                                                                                           Claim 2; Page 55; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        degeneracy of the DNA sequences.
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                                            WPI; 2002-097764/13.
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 AA;
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Nicolette CA;
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAC97991 to AAC98763 encode the human colon cancer associated proteins, called human colon cancer antigens, given in AAB53234 to AAB54006. The human colon cancer antigens can have cytostafic, cardioactive, muscular; human colon cancer antigens can have cytostafic, cardioactive, muscular; culnerary, nephrotropic, antiinfective and antibacterial activities, and can be used in gene therapy. The colon cancer antigen polymucleotides, proteins and antibodies to the proteins are useful for the prevention, treatment and diagnosis of colon disorders, such as colon cancer. The polymucleotides may be used in diagnostics and research, such as for chromosome identification, and as hybridisation probes. The proteins may also be used to prevent disorders, reproductive disorders, immune system disorders, muscular disorders, reproductive disorders, immune gastrointestinal disorders, wounds, renal disorders, infectious diseases, and cardiovascular disorders. AAC987764 to AAC98772 and AAC98707 represent sequences used in the exemplification of the present
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                                                                                                                 Colon cancer associated gene sequences, referred to as colon cancer antigens, useful for the treatment, prevention, and diagnosis of colon
                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                   80.0%; Score 40; DB 21; Length 148; 100.0%; Pred. No. 7; or Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human protein sequence SEQ ID NO:12932.
                                                                                                                                                           Claim 11; Page 1356; 2104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB93552 standard; Protein; 528 AA.
                                                                                                                              antigens, useful for the treatmer
disorders such as colon cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
                                          (HUMA-) HUMAN GENOME SCI INC
                     99US-0124270.
08-MAR-2000; 2000WO-US05883.
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Best Local Similarity 100.
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                                                                Rosen CA, Ruben SM;
                                                                                    WPI; 2000-587534/55.
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                                                                                                                                                                                                                                                                                                                                                                 148 AA;
                                                                                             N-PSDB; AAC98017.
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                     12-MAR-1999;
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11-JAN-2000;
02-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                             invention.
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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonuclectide complementary complementary strand of a polynucleotide which comprises one of the 5602 nucleotide comprises at least 15 nucleotides; or (b) a combination of alignoucleotide comprises a sequence complementary to the complementary strand of a polynucleotide which comprises a 3'-end sequence complementary to the sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence complementary to a complementary strand of a polynucleotide which comprises a 1-end sequence complementary to a polynucleotide comprises at 1-east 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the becinitation. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs assily without any specialised methods. AAH13618 and AAH13631 to AAH13632 to AAH13632 to passent thuman amino acid sequences; and AAH13629 to AAH13632 represent invention.
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                                                                                                                                                                                      Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
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           Saito K, Yamamoto J;
Otsuki T;
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                                                                                                                                                                                                                                                                                                                                                                     Claim 8; SEQ ID 12932; 2537pp + CD ROM; English.
       hikawa T, Hayashi K, S
Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Prec. ...
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Isogai T, Nishikawa T,
Sugiyama T, Wakamatsu
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27-APR-2000; 2000US-0560875.
20-JUN-2000; 2000US-0598075.
19-JUL-2000; 2000US-0620325.
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                                                                                                              WPI; 2001-318749/34
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                                                                                                                                                                                                                                                                                                 Full-length cDNAs
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   Ota T, Is
Ishii S,
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WPI; 2001-007395/01.
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                                                                                                                                      735 AA;
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N-PSDB; AAF81521.
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Azimzai Y;
                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                      AAB27226;
                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                RESULT 7
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                                                                                                                                                                                   The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80102) that exhibit activity elating to erytokine, cell proliferentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hemantopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or
                                                                 Ma Y;
                                                                                                                                                                                                                                                                             treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                             Note: Records for SEQ ID NO 2110 (AAKS2581), 2111 (AAKS2582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               muskelin; AIDS; retrograde neuropathy; topical anaemic damage; development deficiency; osteopathy.
                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                     Nucleic acids encoding polypeptides with cytokine-like activities
                                                                 Cao Y,
                                                                                                                                                                                                                                                                                                                                                                             ;
                                                              Drmanac RT, Asundi V, Zhou P, Xu C, Ca
Wang J, Zhang J, Ren F, Chen R, Wang
Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                        80.0%; Score 40; DB 22; Length 735; 100.0%; Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                 100.0%; Preu. ....
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                                                                                                                                                                  Claim 20; Page 4349-4350; 6221pp; English
                                                                                                                                              useful in diagnosis and gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB73094 standard; Protein; 735 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-SEP-2000; 2000WO-CN00269.
01-SEP-2000; 2000US-0654936.
15-SEP-2000; 2000US-0653561.
20-OCT-2000; 2000US-0693325.
30-NOV-2000; 2000US-0728422.
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Best Local Similarity 100.
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                                                                                                       WPI; 2001-476283/51
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                                                                Liu C, D
Wang D,
Yang Y, W
                                                                                                                                                                                                                                                                                                                                                                                               2 LHKVHYL 8
                                                                                                                                                                                                                                                                                                                                       735 AA;
                                              (HYSE-) HYSEQ INC.
                                                                                                                 N-PSDB; AAK52414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human muskelin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-SEP-1999;
                                                                                                                                                                                                                                                                                      inflammation.
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                                                                 Tang YT,
Zhao QA,
                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                     Kue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          spinal
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                                                                                                                                                                                                    The present invention provides the protein and coding sequences of a novel human muskelin. The sequences are useful in the treatment of acquired immunodeficiency syndrome (AIDS), retrograde neuropathy, spinal development deficiency, topical anaemic damage, osteopathy, malignant tumours and chronic infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention provides the protein and coding sequences for 25 novel extracellular matrix and adhesion-associated proteins (EXMADS). These are designated EXMAD-1, EXMAD-2, EXMAD-3, EXMAD-4, EXMAD-5, EXMAD-1, EXMAD-10, EXMAD-11, EXMAD-13, EXMAD-13, EXMAD-14, EXMAD-16, EXMAD-17, EXMAD-17, EXMAD-17, EXMAD-21, EXMAD-21, EXMAD-21, EXMAD-22, EXMAD-23, EXMAD-22, They are useful in the prevention and treatment of cancers, cell proliferation,
                                    topical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Extracellular matrix and adhesion-associated protein; EXWAD; cancer; inflammation; reproductive disorder; cardiovascular disorder; immune disorder; musculoskeletal disorder; developmental disorder; gastrointestinal disorder; cell proliferation disorder.
New muskelin polypeptide, for treating acquired immunodeficiency syndrome, retrograde neuropathy, spinal development deficiency, to anemic damage, osteopathy, malignant tumor and chronic infections
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80.0%; Score 40; DB 22; Length 735; 100.0%; Pred. No. 37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB27226 standard; Protein; 735 AA.
                                                                                                                                             Claim 1; Page 21-23; 27pp; Chinese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .0-MAY-2000; 2000WO-US12811.
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99US-0150409.
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Matches 7; Conservative
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99US-0147192.
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14.7UN-1999;
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musculoskeletal, developmental and
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                                     Query Match 80.0%; Score 40; DB 22; Length 735; Best Local Similarity 100.0%; Pred. No. 37; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                               Arabidopsis thaliana protein fragment SEQ ID NO: 27656.
cardiovascular, reproductive, immune, muscu
gastrointestinal disorders and inflammation
                                                                                                                               AAG24107 standard; Protein; 127 AA
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990S-0123180.
990S-0123180.
990S-0125788.
990S-0126765.
990S-0126783.
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990S-0130871.
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|HKVHYL 600
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                        735 AA;
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      1; Mismatches
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99US - 0123180 .
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      6; Conservative
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22-0CT-1999
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25-0CT-1999
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25-0CT-1999
26-0CT-1999
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DB 21; Length 127; 33;

Score 36; Pred. No.

72.0%; 75.0%;

Query Match Best Local Similarity

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Query Ma
Best Loc
Matches
   8 6
990S-0139453.
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990S-0144836.
990S-0144838.
990S-0144838.
990S-0145918.
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23 - JUL - 1999;
23 - JUL - 1999;
24 - JUL - 1999;
27 - JUL - 1999;
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29 - JUL - 1999;
20 - AUG - 1999;
30 - AUG - 1999;
 16-70N-1999,
17-70N-1999,
18-70N-1999,
23-70N-1999,
23-70
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Gaps ö Length 321; Indels ö 21; Score 36; DB : Pred. No. 87; 2; Mismatches 2; 990S - 0148565 - 990S - 0148565 - 990S - 01485684 - 990S - 0149368 - 990S - 0149175 - 990S - 0149175 - 990S - 0149175 - 990S - 0149172 - 990S - 0149172 - 990S - 0149723 - 990S - 0149929 - 990S - 015929 - 990S - 0151303 - 990S - 0151333 - 990S - 015929 - 990S - 01691405 - 990S - 0161405 - 990S - 0161405 - 990S - 0161405 - 990S - 0161405 - 990S - 0161350 - 990S - 0161352 -Similarity 71.4%; 5; Conservative 38 Φ ||:||:| 32 HKIHYVV з нкинуги 13-AUG-1999 13-AUG-1999 14-AUG-1999 20-AUG-1999 20-AUG-1999 20-AUG-1999 20-AUG-1999 21-AUG-1999 22-AUG-1999 22-AUG-1999 22-AUG-1999 22-AUG-1999 22-AUG-1999 23-AUG-1999 24-SEP-1999 25-AUG-1999 26-CCT-1999 26-CCT-1999 27-AUG-1999 28-SEP-1999 28-SE Match Local S

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990S - 0.1452176
990S - 0.145918
990S - 0.145918
990S - 0.145951
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990S - 0.146386
990S - 0.146386
990S - 0.14738
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99US-0145192.
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99US-0149723
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08-JUL-1999;
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28-JUL-1999;
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19-JUL-1999;
  Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                 Arabidopsis thaliana protein fragment SEQ ID NO: 28130
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990x5-0123180.
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990x5-0126264.
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05-MAR-1999;

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25-MAR-1999;

25-MAR-1999;

01-APR-1999;

06-APR-1999;

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23-APR-1999;

23-APR-1999;

06-MAY-1999;

06-MAY-1999;

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06-MAY-1999;

06-MAY-1999;
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1-JUN-1999;
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-MAY-1
-MAY-1
   RESULT 10
                AAG24453
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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990S - 0125788
990S - 0126785
990S - 0120845
990S - 0120845
990S - 0130849
990S - 0130891
990S - 0130891
990S - 0130891
990S - 0132486
990S - 0134218
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99US-0139452.
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99US-0139454.
99US-0139455.
99US-0139456.
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99US-0139460.
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18-JUN-1999;
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28-APR-1999;
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14-MAY-1999;
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27-MAY-1999;
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0
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Pred. No. 89;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAG06847 standard; Protein; 378 AA.
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Best Local Similarity 75.0%;
Matches 6; Conservative
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FLHKIHRL 59
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ID AAGC
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AC AAGC
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DT 17-C
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Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 36; DB 21; Length 378; Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Listeria monocytogenes protein #932.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB48228 standard; Protein; 454 AA.
990S-0151080
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990S-0151303
990S-0151303
990S-0153758
990S-0153758
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71.4%;
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99US-0161405
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89 HKIHYVV 95
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Best Local Similarity
Matches 5; Conserv
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27-AUG-1999;
30-AUG-1999;
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Listeria monocytogenes

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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 17976; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster polypeptide SEQ ID NO 24660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 36; DB 22;
Pred. No. 2.8e+02;
2; Mismatches 0;
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                                                                                                                                                                                                                                              Myers EW
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                                                                                                                                                                                                                                              PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72.0%;
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                                                                                       23-MAR-2001; 2001WO-US09231
                                                                                                                                23-MAR-2000; 2000US-191637P.
                                                                                                                                                     11-JUL-2000; 2000US-0614150
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11-JUL-2000; 2000US-0614150.
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Best Local Similarity 71.*
Series 5; Conservative
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                                                                                                                                                                                                                                            Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adams M,
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WO200171042-A2
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                                           27-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to the genome sequence of Listeria monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of it are useful for selecting probes and primers for detecting genes in L. monocytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein encoded by the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, and for biosynthesis and biodegradation, especially biosynthesis of Vitamin B12. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate L. monocytogenes-related diseases. In addition, the genome compositions for the treatment or prevention of infections by L. monocytogenes and related organisms.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                       Dehoux P;
Cossart P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related bacterial infections, and related polypeptides
                                                                                                                                                                                                                                   Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P, Dussurget O, Cherouani F, Nedjari H, Glaser P, Kunst F, Cossart E Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA, Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A, Chakraborty T, Domann E, Hahn T, Berche P, Chakrabit A, Durant L, Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N, Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster polypeptide SEQ ID NO 17976.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 6; SEQ ID No 933; 192pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB63728 standard; Protein; 979 AA.
                                                                                                       11-APR-2001; 2001WO-FR01118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                11-APR-2000; 2000FR-0004629
                                                                                                                                                                                                                                                                                                                     Chakraborty T, Domann E,
Perez-Diaz J, Baquero F,
Maduenio E, De Pablos B,
Rose M, Voss H;
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239 YLHKLHY 245
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                                                                                                                    The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; cancer antigen; ATF4; CREB-2; vaccine; cytostatic; immunogenic ligand; gene therapy; MHC; major histocompatibility complex; adoptive immunotherapy; cancer; ovarian cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to compounds comprising an immunogenic ligand whose sequence is based in part on residues 42-50 of human cancer antigen ATF4/CREB-2 (not defined) and the polynucleotides encoding them.
                                                                                                                                                                                                                                   The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                      New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New therapeutic compounds comprising immunogenic ligands, useful for modulating an immune response, particularly for treating ovarian cancer, and as components of anticancer vaccines -
                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                              Disclosure; SEQ ID NO 24660; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                        72.0%; Score 36; DB 22; Length 1084; 55.6%; Pred. No. 3.1e+02; tive 3; Mismatches 1; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human cancer antigen ATF4/CREB-2 based immunogenic ligand #3.
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20-DEC-2000; 2000US-257007P.
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345 FLHNLHHLI 353
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WPI; 2001-656860/75.
N-PSDB; ABL10059.
                                                                                                                                                                                                                           (ABB57737-ABB72072)
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                                                                     interactions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
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compound, a method for inducing an immune response in a subject by delivering the compound, a method of immunor response in a subject by delivering the compound, a method of immunorherapy comprising delivering to a subject the antibody, an immune effector cell that has been raised in vitro or in vivo in the presence and at the expense of an antigen presenting coll that presents the immunogenic compound in the context of an MHC (major histocompatibility complex) molecule and a method of adoptive immunotherapy comprising administering the immune response to the synthetic and naturally occurring compounds. The compounds are specially useful in gene therapy or as components of anti-cancer vaccines. The compounds are useful for treating cancer, particularly covarian cancer. The compounds are also useful for generating antibodies that specifically recognise and bind to these molecules. These compounds are also useful for generating antibodies that specifically recognise and bind to these molecules. These subject. The peptides, polypeptides and polynuclectides are useful in diagnostic methods, for the detection and purification of antibodies. The present can as immunogens for the production of antibodies. The present immunogenic sequence represents a human cancer antigen ATF4/CREB-2 based immunogenic
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FLHKWHWVV
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52, Appl 2, Appli 3, Appli 7436, Ap 3, Appli 33130, Ap 4407, Appli 111, App

Sequence Sequence Sequence

Sequence

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US-07-752-101A-38
US-07-752-101A-39
US-07-752-101A-51
US-07-752-101A-51
US-07-752-101A-52
US-07-841-651-2
US-07-841-651-2
US-07-841-651-3
US-09-328-352-7436
PCT-US44-00198-3
US-09-328-352-4407
US-08-484-905-111
US-08-481-905-111
US-08-370-476-111
US-08-376-255-13
US-09-739-455-7
US-09-739-455-7
US-09-134-001C-3112
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 36, Application US/08378939
Patent No. 5876961
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 6; Conservative
   TOPOLOGY: linear

HOLECULE TYPE: protein

US-08-378-939-36
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Sequence 5000, App
Sequence 1, Appli
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Sequence 7, Appli
Sequence 7331, Appli
Sequence 7331, Appli
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19, Appl
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63, Appl
63, Appl
63, Appl
3, Appli
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13, Appli
1619, Ap
                                                                                                         December 16, 2003, 14:11:00; Search time 12.3333 Seconds (without alignments) 30.875 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 13, R
Sequence 1619,
Sequence 68, R
Sequence 2901
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Sequence
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
             GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-215-694-7

US-09-318-352-7101

US-09-328-352-7101

US-09-328-352-7331

US-08-24-125-19

US-09-126-420A-20

US-09-499-302A-7

US-09-499-302A-7

US-08-477-346-63

US-08-477-346-63

US-08-477-346-63

US-08-477-346-63

US-08-477-346-63

US-08-477-346-63

US-08-477-346-63

US-08-477-346-63

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US-09-732-10-1619
US-09-752-101A-68
US-09-252-991A-29014
US-09-328-352-5381
US-09-107-52A-4118
US-07-752-101A-35
US-07-752-101A-35
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US-09-134-001C-5000
                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                      328717 seqs, 42310858 residues
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                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                             OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                        US-09-870-089B-11
50
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length: 2000000000
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Match Length DB
                                                                                                                                                                                                         1 FLHKVHYLV 9
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq
Maximum DB seq
                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database
                                                                                                             Run on:
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No.
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Sequence
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,939
FILING DATE: US/08/378,939
FILING DATE: US/08/378,939
FILING DATE: US/08/378,939
ATTORNEY/AGENT INFORMATION:
FILING DATE: U-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: ERNST, BARBARA G
REGISTRATION NUMBER: 30,377
REPRENCE/DOCKET NUMBER: 30,377
REPRENCE/DOCKET NUMBER: 1808-118
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: CROWE, JAMES SCOTT
APPLICANT: LEWIS, ALAN PETER
TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
STREET: 555 THRIEBENTH ST. N.W.
CITY MASHINGTON
STATE: D. C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72.0%; Score 36; DB 2; 100.0%; Pred. No. 16;
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                                                                                                                     68.0%; Score 34; DB 1; Length 311; 71.4%; Pred. No. 94;
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                                                                                                                                                                                                                                                                                                    RESULT 4
US-09-100-851-1
Sequence 1, Application US/09100851
Patent No. 5911984
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Purvi,
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN PEROXISOMAL THIOESTERASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE:
                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/872,784
APPLICATION NUMBER: US/08/872,784
FILING DATE:
ATTORNY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION WUMBER: 36,749
REFERENCE/DOCKET NUMBER: 9F-0293 US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 1, Application US/09265294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY.

ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
TYPE: IBM Compatible
TYPE: TEM Compatible
TYPE: TEM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 311 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                Query Match
Best Local Similarity 71.4"
For Si Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
             IMMEDIATE SOURCE:
LIBRARY: BRAINOT09
CLONE: 2150905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIBRARY: BRAINOT09
CLONE: 2150905
                                                                                                                                                                                                                                 239 HKVHFMV 245
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239 HKVHFMV 245
linear
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Matches 5; Conserv
                                                               ; CLONE: ;
US-08-872-784-1
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US-09-265-294-1
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                                                          Sequence 5000, Application US/09134001C

Patent No. 6380370
GENERAL INFORMATION:
FALENCE OF INVENTION:
FILE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
FRIOR PEDICATION NUMBER: US 60/064,964
FRIOR FILING DATE: 1997-11-08
FRIOR PEDICATION NUMBER: US 60/055,779
FRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 5000
LENGTH: 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 35; DB 4; Length 190;
Pred. No. 39;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Pur'al
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN PEROXISOMAL THIOESTERASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
OFFRATING SYSTEM: DOS
SOFTWARE: FastSRQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/872,784
FILING DATE: Filed Herewith
PKIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5000
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FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE DOCKET NUMBER: PP-0.
TELECOMMUNICATION INFORMATION:
TT.RPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-872-784-1; Sequence 1, Application US/08872784; Patent No. 5776753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70.0%;
55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :|||:::||
114 YLHKINFLV 122
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Best Local Similarity
Matches 5; Conserv
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Length 1068;
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68.0%; Score 34; DB 4; Length 106 ilarity 71.4%; Pred. No. 3.1e+02; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 50.0
Matches 4; Conservative
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Matches 4; Conservative
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116 FMHEIHALI 124
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185 FLHRVHH 191
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71 IHKAHYIL 78
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Query Match
Best Local Similarity
Matches 5; Conserv
                                                                         1 FLHKVHY 7
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TYPE: PRT
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Patent No. 6391581
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wisconsin Alumni Research Foundation
APPLICANT: Hutchinson, Charles R.
APPLICANT: Kennedy, Jonathan n.m.i
APPLICANT: Park, Checonseck n.m.i
ITILE OF INVENTION: METHOD OF PRODUCING ANTHYPERCHOLESTEROLEMIC AGENTS
FILE REFERENCE: 960296.95718
CURRENT APPLICATION NUMBER: 1999-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Pred. No. 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                 APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN PEROXISOMAL THIOESTERASE
CORRESPONDENCE: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                               SOFTWARE: FASTEM: DOS
SOFTWARE: FASTEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/265,294
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                             ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF-0293 US
                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,851
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFRENCE/DOCKET NUMBER: PF-02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-85-055
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LENGTH: 1068
; TYPE: RRT
; ORGANISM: Aspergillus terreus
US-09-215-694-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         311 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 71...
hea 5; Conservative
                                                                                                                                                                                                                                       ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BRAINOT09
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239 HKVHFMV 245
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SOFTWARE: Patentin Ve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                 STREET: 3174 Por
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIBRARY: BKALLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 НКУНУЦУ 9
Patent No. 6210890
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMMEDIATE SOURCE
                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6
US-09-215-694-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-265-294-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
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US-09-328-352-7101
US-09-328-352-7101
Sequence 7101, Application US/09328352
Fatent No. 6562958
GENERAL INFORMATION:
TYPICANT: GATY L. Breton et al.
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION UNMER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NOS: 8252
TENNOM: 7.01
TENNOM: 7.01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 731, Application US/09328352
Patent No. 6562958
Patent No. 6562958
Patent No. 6562958
Patent No. 6562958
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REPERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7331
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Patent No. 5744341
Genent No. 5744341
GENERAL INFORMATION
APPLICANT: CUNINGHAM JR., FRANCIS X.
APPLICANT: SUN, ZAIREN
ITILE OF INVENTION: GENES OF CAROTENOID BIOSYNTHESIS AND
ITILE OF INVENTION: METABOLISM AND A SYSTEM FOR SCREENING SUCH GENES
NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
Gaps
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KELBER, STEVEN B.
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LENGTH: 471
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Sequence 19, Application US/08937155

Sequence 19, Application US/08937155

Sequence 10, 6524811

GENERAL INFORMATION:
APPLICANT: CUNNINGHAM JR., FRANCIS X.
APPLICANT: SUN, ZAIREN

TITLE OF INVENTION: GENES OF CAROTENOID BIOSYNTHESIS AND
TITLE OF INVENTION: METABOLISM AND A SYSTEM FOR SCREENING SUCH GENES
NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66.0%; Score 33; DB 1; Length 288; 50.0%; Pred. No. 1.3e+02; tive 4; Mismatches 0; Indels
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,155
                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/624,125
FILING DATE: 29-MAR-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: KELBER, STEVEN B.
REGISTRATION NUMBER: 30,073
REFERENCE/DOCKET NUMBER: 2747-063-27
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/624,125
FILING DATE: 29-WAR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER REDDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS: LENGTH: 288 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||:::||:
189 FLNRIHYM 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 4; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 FLHKVHYL 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-624-125-19
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APPLICANT: BATARD, YANNICK
APPLICANT: BATARD, YANNICK
APPLICANT: BATARD, YANNICK
APPLICANT: BATARD, YANNICK
APPLICANT: ROBINEAU, TIBURCE
APPLICANT: DIDERLEADAN, LUC
TITLE OF INVENTION: TUBERCOSUS AND ITS APPLICANTS DIVENTION: TUBERCOSUS AND ITS APPLICANT DIDERLEADAN, LUC
TITLE OF INVENTION: TUBERCOSUS AND ITS APPLICATIONS AS BIOCATALYST IN
TITLE OF INVENTION: POLLUTANTS AND FOR ALTERING THE RESISTANCE OF PLANTS S
FILE REFERENCE: 03715.0032
CURRENT FILING DATE: 1998-07-30
PRIOR PILING DATE: 1999-07-31
PRIOR PELLING DATE: 1997-07-31
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APPLICANT: BOUNG-JUN, OH
APPLICANT: MOON, KYUNG KO
TITLE OF INVENTION: A CYTOCHROME P450 GENE HIGHLY EXPRESSED IN THE
TITLE OF INVENTION: INCOMPATIBLE INTERACTION
FILE REPERRNCE: 10324/64443USO
CURRENT APPLICATION NUMBER: US/09/499,302A
                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                          Length 288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 471;
                                                                                                                                                                                                                                                                                           Score 33; DB 4; Lengtn 2007, Pred. No. 1.3e+02;
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Best Local Similarity 71.4%; Pred. No. 2.1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                    4; Mismatches
                                 2747-063-27
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REGISTRATION NUMBER: 30,073
REFERENCE/DOCKET NUMBER: 2747
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3200
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                             66.0%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.1
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Best Local Similarity 50.v.
--- 4; Conservative
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ORGANISM: Persea americana
                                                                                                                                                                                                                        ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-937-155-19
                                                                                                                                                                                                     STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                         ||:::||:
189 FLNRIHYM 196
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                                                                                                                                             66.0%; Score 33; DB 1; Length 713; 75.0%; Pred. No. 3.1e+02; tive 1; Mismatches 1; Indels
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Patent No. 6362023

GRBRAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Doritt
TITLE OF INVENTION: Thereof
ITILE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Poerster
STREET: 2000 Pennsylvania Avenue, NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,802A
FILING DATE: 01-FEB-1994
CLASSIFCATION: 530
ATTORNEY/AGENT INFORMATION:
NUMBE: Fabian, Gary R.
REGISTRATION NUMBER: 8600-0139
REFERENCE/DOCKET NUMBER: 8600-0139
TELEPHONE: (415) 324-0860
TELEPHONE: (415) 324-0960
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYDOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: TUP1, Fig. 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 713 amino acids
amino acid
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Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            279 LHQDHYLV 286
                                                    259 LHQLHYL 265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 94306-0850
                            2 LHKVHYL
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US-08-477-346-63
                                                                                                                                                                                                                                                                                                                                                                                                         CITY:
STATE:
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Sequence 2105.74
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: MUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 23106
LENGTH: 554
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h 66.0%; Score 33; DB 4; Length 502; Similarity 71.4%; Pred. No. 2.2e+02; 5; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (199)
OTHER INFORMATION: variable or unknown amino acid
NAMB/KEY: NOD RES
LOCATION: (126)
OTHER INFORMATION: variable or unknown amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (240)
OTHER INFORMATION: variable or unknown amino acid
NAME/KEY: MOD RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (247)
OTHER INFORMATION: variable or unknown amino acid
MAME/KEY: MOD_RES
LOCATION: (262)
OTHER INFORMATION: variable or unknown amino acid
                                                                                                                                                                                                                                                                                           LOCATION: (30)
OTHER INFORMATION: variable or unknown amino acid
NAME/KEY: MOD RES
LOCATION: (49)
                                                                                                                                                                                                                                                    OTHER INFORMATION: variable or unknown amino acid NAME/KEY: MOD_RES
                                                                                                                                                                                         OTHER INFORMATION: variable or unknown amino acid
                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: variable or unknown amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: variable or unknown amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Pseudomonas aeruginosa
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 7
LENGTH: 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        349 LHQLHYL 355
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Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 LHKVHYL 8
                                                                                       TYPE: PRT
ORGANISM: Persea sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: MOD RES
LOCATION: (240)
                                                                                                                                                NAME/KEY: MOD_RES
LOCATION: (1)
                                                                                                                                                                                                             NAME/KEY: MOD_RES
LOCATION: (22)
                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: MOD RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: MOD RES
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Query Match 66.0%; Score 33; DB 3; Length 713; Best Local Similarity 75.0%; Pred. No. 3.1e+02; Matches 6; Conservative 1; Mismatches 1; Indels
CITY: Washington
STATE: DC
CONDTRY: USA
ZID: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,346
FILING DATE: 07-JUN-1995
ATTORNEY/ASMY INFORMATION: 514
PRIOR APPLICATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 79,959
REFERENCE/DOCKET NUMBER: 79,959
REFERENCE/DOCKET NUMBER: 70,919
REFERENCE/DOCKET NUMBE
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Search completed: December 16, 2003, 14:20:41 Job time : 13.3333 secs

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Gaps 0;

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probable CHP-rich
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G protein-coupled
cytochrome P-450LX
                                                        probable CHP-rich
probable CHP-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein DKPZp7621156.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Species: T47173
R;Bloecker, H.; Boecher, M.; Brandt, P.; Mewes, H.W.; Weil, B.; Wiemann, S. submitted to the Protein Sequence Database, March 2000
A,Reference number: Z24376
A,Reference number: Z24376
A,Recession: T47173
A,Status: preliminary
A,Rolecule type: mRNA
A,Residues: 1-416 <AAA>
A,Residues: 1-416 <AAA>
A,Residues: 1-416 <AAA>
A,Coss-references-FEMBL:AL162071
A,Experimental source: adult melanoma (MeWo cell line); clone DKFZp7621156
                                         1-coumarate-CoA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80.0%; Score 40; DB 2; Length 416, 100.0%; Pred. No. 4.7; o; Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                A34440
T29416
A35867
T31717
T34193
                                                                                              T02001
F85024
T10575
                                                        E85024
G85024
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C82714
                                         F03390
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Best Local Similarity 100.
Matches 6; Conservative
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C, Genetics:
A, Nore: DKFZp7621156.1
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RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                        (without alignments)
83.760 Million cell updates/sec
                                                                                                                                      2003, 14:10:15 ; Search time 10.3333 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
                  GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                         283308 seqs, 96168682 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                              OM protein - protein search, using sw model
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F30534
KVMS7A
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Gapop 10.0 , Gapext 0.5
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1 FLHKVHYLV 9
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seq length: 200000000
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                                   Copyright
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Database

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A;Accession: D3538
A;Status: preliminary: nucleic acid sequence not shown; not compared with conceptual transportations: preliminary: nucleic acid sequence not shown; not compared with conceptual transportations: 12-104 cCL7>
A;Residues: 32-104 cCL7>
A;Residues: 32-104 cCL7>
A;Experimental source: 253.1265
A;Experimental source: 253.1265
Lain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology cIMM>
F;16-96/Domain: immunoglobulin homology cIMM>
F;23-94/Disulfide bonds: #status predicted
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C'Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
C;Accession: C85431
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprir: Nature 402, 769-777, 1999
                                                                                       A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Experimental source: clone 224.7B7
A;Accession: C30538
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aritle: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana. A, Reference number: A85001; MUID:20083488; PMID:10617198
A, Accession: C85431
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                                                                                                                                                                                               A;Residues: 1-106 <CLA>
A;Residues: 1-106 <CLA>
A;Rxperimental source: clone 252.5E10
A;Accession: 1030534
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-104 <CL2>
A;Experimental source: clone 224.2B8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: E30534
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-113 <CL3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Experimental source: clone 224.2G3
A;Accession: G30534
A;Status: preliminary; not compared with conceptual translation
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A;Reference number: A30534; MUID:89035545; PMID:3141511
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A;Experimental source: clone 252.5E11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-105 <CL4>
A;Experimental gource: clone 224.1C7
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A;Molecule type: DNA
A;Residues: 1-378 <STO>
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A;Map position: 4
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C;Species: Mus musculus (house mouse)
C;Date: 10-Feb-1989 #sequence_revision 10-Feb-1989 #text_change 21-Jan-2000
C;Date: 10-Feb-1989 #text_change
                                                                                                                                                                     Ig kappa chain V region (224.4B11) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 10-Peb-1989 #sequence_revision 10-Feb-1989 #text_change 21-Jan-2000
C;Date: 11-Relian, J.L.; Berry, J.
R;Claflin, J.L.; Berry, J.
J. Immunol. 141, 4012-4019, 1988
A;Title: Genetics of the phosphocholine-specific antibody response to Streptococcus pneu A;Reference number: A30534; MUID:89035545; PMID:3141511
A;Accession: H3053
A;Accession: H3053
A;Accession: Miscalanianary
A;Residues: 1-113 <CLA>
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C.Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;16-96/Domain: immunoglobulin homology <IMM>

A; Residues: 1-113 <CLA>

72.0%; Score 36; DB 2; 100.0%; Pred. No. 6.9; iive 0; Mismatches

6; Conservative

34 HKVHYL 39

3 НКУНУІ 8

Query Match Best Local Similarity Matches 6; Conserv

Ig kappa chain V region (S107A) - mouse

RESULT 5 KVMS7A

A; Accession: A01915

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Indels

72.0%; Score 36; DB 2; Length 113; 100.0%; Pred. No. 6.9;

0; Mismatches

6; Conservative

34 HKVHYL 39

d ò

3 HKVHYL 8

Best Local Similarity Matches 6; Conserv

Query Match

Residues: 1-113 <CLA> Superfamily: immunoglobulin V region; immunoglobulin homology Keywords: heterotetramer; immunoglobulin

C, Superfamily: immuner; immunogicum... C, Keywords: heterotetramer; immunoglobulin homology <IMM> F;16-96/Domain: immunoglobulin homology <IMM>

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Length 378;
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Pred. No. 25;
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71.4%;
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Best Local Similarity
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A/Title: Genetics of the phosphocholine-specific antibody response to Streptococcus pned
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A;Residues: 1-114 <KWA>
A;Note: Les sequency as determined from the differentiated gene
R;Clafilin, J.L.; Berry, J.
J. Immunol. 141, 4012-4019, 1988
Length 113;
                                 0; Indels
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cytochrome C-type biogenesis protein comP (comP) RP703 - Rickettsia prowazekii C;Species: Rickettsia prowazekii C;Species: Rickettsia prowazekii C;Species: Rickettsia prowazekii C;Species: Rickettsia prowazekii C;Accession: C71630
R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, I Nature 396, 133-140, 1998
A;Title: The genome sequence Of Rickettsia prowazekii and the origin of mitochondria. A;Title: The genome sequence Of Rickettsia prowazekii and the origin of mitochondria. A;Reference number: A71630
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Residues: 1-670 <AND>
                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AJ235273; GB:AJ235269; NID:g3861237; PIDN:CAA15139.1; PID:g38612·
A;Experimental source: strain Madrid E
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A;Molecule type: DNA
A;Residues: 1-300 <MCD.
A;Residues: 1-300 <MCD.
A;Cross-references: EMBL.AL108832; PIDN:CAB52730.1; GSPDB:GN00066; SPDB:SPAC630.08c
A;Experimental source: strain 972h-; cosmid c630
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Apportetical protein C0415c - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Species: Plasmodium falciparum
C;Aate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2002
C;Accession: T18438
R;Lawson, D.; Bowman, S.; Barrell, B.
submitted to the EMBL Data Library, August 1997
A;Reference number: Z18935
A;Reference number: Z18935
A;Reference number: Z18935
A;Accession: T18438
A;Accession: T18438
A;Accession: T18438
A;Accession: L18438
A;Residues: 1-1532 < LAW>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 36; DB 2; Length 670;
Pred. No. 47;
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C;Superfamily: Saccharomyces cerevisiae ERG25 protein
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1; Mismatches
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Best Local Similarity 75.0°,
-haq 6; Conservative
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A;Gene: ccmF; RP703
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A; Note: C0415c
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A;Molecule type: DNA
A;Molecule type: DNA
A;Kesidues: 1-454 <GLA>
A;Kesidues: 1-454 <GLA>
A;Cross-references: GB:NC_003210; PIDN:CAC99220.1; PID:gl6410558; GSPDB:GN00177
A;Experimental source: strain EGD-e
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A,Experimental source: strain Clip11262
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Pred. No. 31;
2; Mismatches C
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71.4%; Pred. No. 31;
tive 2; Mismatches (
       Mismatches
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illarity 71.4%;
Conservative :
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Best Local Similarity 71.4
Matches 5; Conservative
       Conservative
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239 YLHKLHY 245
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Best Local Similarity
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239 YLHKLHY 245
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A;Gene: lmo1142
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Best Local Similarity 62.5%;
Matches 5; Conservative
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Best Local Similarity 62.5
Matches 5; Conservative
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970 FLHRLHHL 977
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C;Species: Ciona intestinalis
C;Species: Ciona intestinalis
C;Date: 22-dan-1999 #sequence_revision 22-Jan-1999 #text_change 23-Mar-2001
C;Accession: T00094
R;Ogasawara, M.; Satoh, N.
Submitted to the EMBL Data Library, February 1998
A;Description: Isolation and characterization of endostyle-specific genes in the Ascidia
A;Reference number: Z14109
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                                                                                                                                                                                                                                                           C'Species: Caenorhabditis elegans
C'Date: 15-0ct-1999 #sequence_revision 15-0ct-1999 #text_change 15-0ct-1999
C'Accession: T29415
R;Wilson, R.; Favello, A.; Le, T.T.
submitted to the EMBLD Data Library, April 1997
A;Description: The sequence of C. elegans cosmid F21F8.
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DB 2; Length 300;
                                          0; Indels
                                                                                                                                                                                                                                        hypothetical protein F21F8.9 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                             A;Accession: T29415
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-347 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: T00094
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-650 <OGAL>
A;Cross-references: EMBL:AB010895
A;Experimental source: endostyle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Map position: 5
A;Introns: 67/3; 97/1; 123/2; 215/3; 258/3; 318/1
Score 35; DB Pred. No. 31; 2; Mismatches
Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative
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10 YLHSIHYI 17
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Best Local Similarity
Matches 4; Conserv
                                                                                   1 FLHKVHY 7
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H97834
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Cispecies: Babesia bovis
Cipate: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jun-2000
Ciaccession 13139
Ciraccession 13139
Ribagnara, A.S.; Chansiri, K.
Gene 172, 173-174, 1996
A;Fitle: Sequences upstream and downstream from the glutamine-dependent carbamoyl phosph
A;Reference number: 221005; MUID:96257278; PMID:8654985
A;Accession: T3133
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1645 <BAG>
A;Cross-references: EMBL:U18792; NID:9944893; PID:g619743; PIDN:AAC47302.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Gene: CPSII
C,Superfamily: carbamoyl-phosphate synthase (ammonia); biotin carboxylase homology; carb
C,Superfamily: carbamoyl-phosphate synthase (glutamine-hydrolyzing) small chain homology; trpG
C;Keywords: ligase
F;26-1623/Domain: carbamoyl-phosphate synthase (ammonia) homology <CPA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 carbamoyl-phosphate synthase (glutamine-hydrolyzing) (EC 6.3.5.5) III - Babesia bovis
Science 293, 2093-2098, 2001
A,Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A,Reference number: A97700, MUID:21442074; PMID:11557893
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A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-662 < KUR>
A; Cross-references: GB: AE006914; PIDN: AAL03618.1; PID: g15620202; GSPDB: GN00173
C; Genetics:
A; Gene: comF
C; Superfamily: nrfE protein
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Pred. No. 1.9e+02;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                        Score 35; DB 2; Length 662;
Pred. No. 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
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RX MEDLINE=2238827; PubMed=12477932;
RA MEDLINE=238827; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Altaner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altachul S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhat N.K.,
RA Altachul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abrameon R.D., Mullahy S.J.,
RA Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzhy D.W., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Schnerch A., Schmutz J., Myers R.M.,
RA Schnerch A., Schmutz J., Marra M.A.;
RA Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
R Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                               neisseria g
neisseria m
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                                                                 homo sapien
                                                                                                 brugia paha
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                                gallus gall
guillardia
                                                                             synechocyst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUBERAIN, Kidney, Lung, and Osteosarcoma;
MEDLINE=20108780; PubMed=10640805;
Adams J.C., Zhang L.,
"CDNA cloning of human muskelin and localisation of the muskelin
(MKIM1) gene to human chromosome 7q32 and mouse chromosome 6 B1/B2 by
physical mapping and FISH."
Cytogenet. Cell Genet. 87:19-21(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Placenta;
Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Nishikawa T., Nagai K., Sugano S., Ishibashi T., Fujimori K.,
Tanai H., Kimata M., Watanabe M., Hiraoka S., Ishii S., Kawai Y.,
Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K.,
Masuho Y., Kanehori K.;
"NEDO human cDNA sequencing project.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
             P08553
P16053
O78441
P07197
P73505
P41959
O007813
Q9ju24
Q9ju24
Q9ju24
Q101322
P19654
                                                                                                                                                                                                                                                                                                                             O9UL63; O9NSK4; O9NUS8;
28-FEB-2003 (Rel. 41, Created)
FFEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last amnotation update)
                                                                                                                                                                                                                                                                                                               735 AA
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                              NFM CHICK
SECA GUITH
NFM HUMAN
                                                                              SYI SYNY3
RS26 BRUPA
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REPL BPP1
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09kuz2 vibrio chol
08dcl6 vibrio vafin
P4477 haemophilus
09c1n8 pageteurella
087172 yfbrio para
08zbgł yerginia pe
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                                                                                                                             (without alignments)
74.689 Million cell updates/sec
                                                                                                             December 16, 2003, 14:06:35; Search time 5.66667 Seconds
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Q42982
Q9h2c0
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               GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                            127863 seqs, 47026705 residues
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RS6 YERPE
RS6 ECOL6
RS6 SALTY
RS6 ECOLI
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HMDH ASPTE
RSG BUCBP
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MKLN MOUSE
MKLN RAT
KV1A MOUSE
RV1A MOUSE
RSE BUCAP
ERSE SCHPO
RSE VIBCH
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Listing first 45 summaries
                                                                              OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                TISSUE-Melanoma;
Bloecker H., Boecher M., Brandt P., Mewes H.-W., Weil B., Wiemann S.;
Submitted (WAR-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Acts as a mediator of cell spreading and cytoskeletal responses to the extracellular matrix component thrombospondin 1
                                                                                                                                                                           (By similarity).

-!- SUBUNIT: Binds with the C-terminal tail of the prostaglandin EP3 receptor alpha isoform (By similarity).
-!- SUBCELULIAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Contains 5 Kelch repeats.
-!- SIMILARITY: Contains 1 LisH domain.
-!- SIMILARITY: Contains 1 CTLH domain.
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Pred. No. 4.1;
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408 I -> N (IN REF. 1).

414 S -> G (IN REF. 1).

436 Q -> K (IN REF. 1).

474 G -> K (IN REF. 1).

502 N (IN REF. 1).

503 N (IN REF. 1).

84767 MW, 1A8F06FEIDE9193D CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AP047489; AAF06698.1; -.
EMBL; AK002024; BAA92042.1; ALT_SEQ.
EMBL; BC002834; AA402834.1; ALT_INIT.
EMBL; AL162071; CAB82407.1; -.
PIR; T47173; T47173.
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InterPro; IPR006595; CTLH.
InterPro; IPR006595; Kelch_rep.
InterPro; IPR006594; LisH.
Pfam; PF01344; Kelch; 3.
SMART; SM00667; CTLH; 1.
PROSITE; PS50897; CTLH; 1.
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(Rel. 41, Last sequ
(Rel. 42, Last anno
  [4]
SEQUENCE OF 320-735 FROM N.A.
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ID MKLN MOUSE

AC 089050;

DT 28-FEB-2003

DT 28-FEB-2003

DT 15-SEP-2003
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     NAMES OF THE STATES OF THE STA
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                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDINE-18741357; PubMed=6788890; MEDINE-81241357; PubMed=6788890; MEDINE-81241357; Rudikoff S., Seidman J.G., Leder P., Scharff M.D.; "Nucleic acid and protein sequences of phosphocholine-binding light
                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                    21-JUJ-1986 (Rel. 01, Created)
21-JUJ-1986 (Rel. 01, Last sequence update)
15-JUJ-1999 (Rel. 38, Last annotation update)
11 Kappa chain V-I region S107A.
Mus musculus (Mouse).
                                                                                                                      114 AA
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                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                          J. Exp. Med. 153:1366-1370(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP, P01675, KWR7A.
HSSP, P01607, IREI.
InterPro; IPR007101, IG-like.
InterPro; IPR003306; IG-MHC.
InterPro; IPR003596; IG-V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immuncglobulin V region.
1
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                                                                                                                    STANDARD;
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594 LHKVHYL 600
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Matches 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34 HKVHYL 39
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                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                    KV1A MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RS6 BUCAP
Q8K918;
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NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                          chains."
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                                                                                                                                  P01632
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                                                                              RESULT 4
KV1A MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 5
RS6_BUCAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND INTERACTION WITH EP3-ALPHA.
MEDDIINE=20462961; PubMed=11006128;
Hasegawa H., Katoh H., Fujita H., Mori K., Negishi M.;
"Receptor isoform-specific interaction of prostaglandin EP3 receptor with muskelin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochem. Biophys. Res. Commun. 276:350-354(2000).
-!- FUNCTION: Acts as a mediator of cell spreading and cytoskeletal responses to the extracellular matrix component thrombospondin 1 (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBUNIT: Binds with the C-terminal tail of the prostaglandin EP3 receptor alpha isoform.
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Contains 5 Kelch repeats.
-!- SIMILARITY: Contains 1 LisH domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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0
                                    80.0%; Score 40; DB 1; Length 735; 100.0%; Pred. No. 4.1; ive 0; Mismatches 0; Indels
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Pred. No. 4.1;
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7B0C8D2CB8C242AA CRC64;
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0
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28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                  735 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 40; DB 101.0%; Pred. No. 4.1 Conservative 0; Mismatches
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KELCH 1.
KELCH 2.
KELCH 3.
KELCH 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interpro; IPR006595; CTLH.
Interpro; IPR006652; Kelch_rep.
Interpro; IPR0066594; LisH.
Piam; PP01344; Kelch; 3.
SMART; SM00668; CTLH; 1.
SMART; SM00667; LisH; 1.
  84877 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AB046442; BAB21439.1; -.
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PROSITE; PS50896; LISH; 1.
                                    Query Match 80.0
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                      594 LHKVHYL 600
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  735 AA;
                                                                                                                  2 LHKVHYL 8
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                  MKLN1 OR MSK.
  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                              Muskelin
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REPEAT
REPEAT
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
305 ribosomal protein S6.
RPSF OR BUGGS44.
Buchnera aphidicola (subsp. Schizaphis graminum).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                    0;
                                           FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
                     COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                            72.0%; Score 36; DB 1; Length 114; 100.0%; Pred. No. 3.3; 0; Mismatches 0; Indels
                                                                                                COMPLEMENTARITY-DETERMINING-3
FRAMEWORK-1.

40 COMPLEMENTARITY-DETERMINING-1
55 FRAMEWORK-2.
62 COMPLEMENTARITY-DETERMINING-2
94 FRAMEWORK-3.
103 COMPLEMENTARITY-DETERMINING-1
113 FRAMEWORK-4.
94 BY SIMILARITY.
114
114
117 MW; 32000BEC8B9DBE67B CRC64;
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Matches

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RS6_VIBCH
ID RS6_VIBCH
AC Q9KUZ2;
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임
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WA MEDLINE=21248401; PubMed=11859360;
WA MEDLINE=21248401; PubMed=11859360;
WA MEDLINE=21248401; PubMed=11859360;
WA Ocd V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sgource J., Peat N., Hayles J., Basham D., Bowaman S., An Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A., Gollins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A., Holroyd S., Hornes D., Hidalgo J., Hodgson G., Holroyd S., Hornes L., Jones M., Leather S., McDonald S., McLean J., Anoney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., Oliver K., O'Neil S., Paarson D., Quail M.A., Rabbinowitsch B., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Woodward J., Volckaert G., As Walsh S.V., Warren T., Whitehead S., Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lab-sib.ch).
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                                                                                        MEDLINE=22084549; PubMed=12089438;
Tamas I., Klasson L., Canbaeck B., Naeslund A.K., Eriksson A.-S.,
Wernegreen J.J., Sandstroem J.P., Moran N.A., Andersson S.G.B.;
"So million years of genomic stasis in endosymbiotic bacteria.";
Science 296:2376-2379(2002).
-i- FUNCTION: Binds together with S18 to 16S ribosomal RNA (By
                                                                                                                                                                                                                                           SIMILARITY; BELONGS TO THE S6P FAMILY OF RIBOSOMAL PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HAMAP; MF 00360; -; 1.

InterPro; IPR00629; Ribosomal S6.

Pfam; PF01250; Ribosomal S6; 1.

ProDom; P0003809; Ribosomal S6; 1.

TIGREAMS; TIGR00166; S6; 1.

PROSITE; PS01048; RIBOSOMAL S6; 1.

Ribosomal protein; TRNA-binding; Complete protecome. SEQUENCE 113 AA; 13501 MW; DEID9286344C1BEC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
EA methyl sterol oxidase (BC 1....).
ERG25 OR SPAC630.08C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 5.1;
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70.0%;
62.5%;
  Enterobacteriaceae; Buchnera
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Best Local Similarity 62.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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                                                                         SEQUENCE FROM N.A.
                             NCBI_TaxID=98794;
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                                                                                                                                                                                                                                        similarity)
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Q9UUH4;
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    HID DIT TO DE STAND THE ST
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MEDLINE=20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P., Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B., Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Shpakovski G.V., Ussery D., Barrell B.G., Nurse P., The genome sequence of Schizosaccharomyces pombe.";
Nature 415:871-880(2002). Gaps -!- PATHWAY: Brgosterol biosynthesis. (Probable). 0; EMBL; AL109832; CAB52730.1; -.
PIR; T38986; T38986.
GeneDB SPombe; SPAC630.08c; -.
InterPro; IPR006089; Sterol_desat.
InterPro; IPR006088; Sterol_desatur.
Pfam; PF01599; Sterol_desat; 1.
Sterol_biosynthesis; Oxidoreductase; Endoplasmic reticulum; Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio. methyl groups of 4,4-dimethylzymosterol (By similarity)
-!- COFACTOR: Iron (By similarity). 70.0%; Score 35; DB 1; Length 300; 71.4%; Pred. No. 14; 0; Indels and/or be involved in metal ion binding. AA8C2603D35DF331 CRC64; HISTIDINE BOX-1. HISTIDINE BOX-2. HISTIDINE BOX-3. 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 28-FRB-2003 (Rel. 41, Last annotation update) 30s ribosomal protein S6. Pred. No. 14; 2; Mismatches 154 158 HI 167 171 HI 251 257 HI 300 AA; 35802 MW; 71.48; Best_Local Similarity 71.4 Matches 5; Conservative STANDARD; 165 FIHKVHH 171 Iron 1 FLHKVHY 7 SEQUENCE FROM N.A. NCBI_TaxID=666; cholerae RPSF OR VC0366.

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InterPro; IPR000529; Ribosomal
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  McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                    "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                           -!- SIMILARITY: BELONGS TO THE SEP FAMILY OF RIBOSOMAL PROTEINS.
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-!- SIMILARITY: BELONGS TO THE S6P FAMILY OF RIBOSOMAL PROTEINS.
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Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Binds together with S18 to 16S ribosomal RNA (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong
Choy H.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68.0%; Score 34; DB 1; Length 122; 62.5%; Pred. No. 8.6; 1; Indels ive 2; Mismatches 1; Indels
                                                                                                             Nature 406,477-483 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGRFAMS; TIGR00166; S6; 1.—
PROSTITE; PS01048; RIBOSOWAL S6; 1.
Ribosowal protein; rRNA-binding; Complete proteome.
SEQUENCE 122 AA; 14249 WW; 4BA3DB6B1FDDBA01 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-SEP-2003 (Rel. 42, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) 30S ribosomal protein S6. RPSF OR VV11387.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000529; Ribosomal S6. Pfam; PF01250; Ribosomal S6; 1. ProDom; PD003809; Ribosomal S6; 1.
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                                                                                                                                                                 (BY SIMILARITY)
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SEQUENCE FROM N.A.
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                                                                                                   cholerae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=Rd / KW20 / ATCC 51907;
MEDLINE=95350630; PubMed=7542800;
MEDLINE=95350630; PubMed=7542800;
MEDLINE=95350630; PubMed=7542800;
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., McKenney K., Lut L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hamma M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                   Gaps
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-!- SIMILARITY: BELONGS TO THE S6P FAMILY OF RIBOSOMAL PROTEINS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
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-!- FUNCTION: BINDS TOGETHER WITH S18 TO 16S RIBOSOMAL RNA
(BY SIMILARITY).
                                                                                                                                                                                                                                  Score 34; DB 1; Length 123; Pred. No. 8.6;
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PROSITE; PS01048; RIBOSOMAL S6; 1.
Ribosomal protein; rRWA-binding; Complete proteome.
SEQUENCE 125 AA; 14484 MW; A3804A2FEFPEBERC CRC64;
                                                                 TIGRFAMS; TIGR00166; S6; 1.—
PROSITE; PS01048; RIBOSOWAL S6; 1.
Ribosomal protein; rRNA-binding; Complete proteome.
SEQUENCE 123 AA; 14301 MW; FCA3C5582FDA3C03 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
RPSF OR RPS6 OR HI0547.
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TIGR; H10547;

TIGR; H0547;

TIRCPPC3: IPR000529; Ribosomal_S6.

Pfam; PF01250; Ribosomal_S6; 1.

ProDom; PD003809; Ribosomal_S6; 1.
Pfam; PF01250; Ribosomal S6; 1.
ProDom; PD003809; Ribosomal S6; 1.
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62.5%;
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Best Local Similarity
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Length 125;

DB 1;

68.0%; Score 34;

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54 LHKAHYVL 61
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            Gaps
                                                                                                                                                                                                                                                                  May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.; "Complete genomic sequence of Pasteurella multocida Pm70."; Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
-!- FUNCTION: BINDS TOGETHER WITH S18 TO 16S RIBOSOMAL RNA (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: BELONGS TO THE S6P FAMILY OF RIBOSOMAL PROTEINS
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                                                                                                                                                                                          Bacteria, Proteobacteria, Gammaproteobacteria, Pasteurellales,
Pasteurellaceae, Pasteurella.
NCBI_TaxID=747;
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Vibrio parahaemolyticus.

Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Vibrio.

Vibrionaceae, Vibrio.

[1]
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Pred. No. 8.8;
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            Indels
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PROSTIR; PSO1048; RIBOSOWAL S6; 1.
RIBOSGOME DYCLEID; TRNA DINGING; COMPLETE DYCLEOME.
SEQUENCE 125 AA; 14505 MW; 102C842FD3FF7736 CRC64;
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                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28 ribosomal protein 86.
RPSF OR RPS6 OR PM1180.
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           2; Mismatches
  Pred. No.
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InterPro; IPR000529; Ribosomal S6.
Pfam; PF01250; Ribosomal S6; 1.
ProDom; PD003809; Ribosomal S6; 1.
                                                                                                                                                                                                                                              STRAIN=Pm70;
MEDLINE=21145866; PubMed=11248100;
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62.5%;
 62.5%;
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           5; Conservative
                                                                                                          STANDARD;
                                                                                                                                                                                   Pasteurella multocida
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LHKAHYVL 61
                                                   54 LHKAHYVL 61
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                                2 ТНКУНУЦУ 9
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                          RS6 PASMU
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                                                                                     RESULT 10
RS6_PASMU
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SERRAIN=CO-92 / Biovar Orientalis;

MEDLINE=1470413; PubMed=11586360;

Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,

Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,

Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,

Baker S., Basham D., Bentley S.D., Brooks K., Cardeno-Tarraga A.M.,

Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,

Feltwell T., Hamlin N., Hollroyd S., Jagels K., Karlyshev A.V.,

Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,

Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.,

"Genome sequence of Yersinia pestis, the causative agent of plague.";

Nature 413:523-527(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=KIMS / Biovar Mediaevalis;
MBDLINE=22137863; PubMed=12142430;
Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P., Perna N.T., Rose D., Plunkett B., Zhou S., Schwartz D.C., Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V., Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
SEQUENCE FROM N.A.

STRAIN=RIND 2210633 / Serotype 03:K6;

MEDLINE=22508454; PubMed=1207039;

MEDLINE=22508454; PubMed=2507039;

Makino K., Oshima K., Kuelokawa K., Yokoyama K., Uda T., Tagomori K., Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S., Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;

"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism distinct from that of V. cholerae.";

Lancet 361:743-749(2003).

-I- FUNCTION: Binds together with S18 to 16S ribosomal RNA (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Yersinia.
                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity).
-!- SIMILARITY: BELONGS TO THE S6P FAMILY OF RIBOSOMAL PROTEINS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BRUDA, MP 00360; -; 1.
PROSITE; PS01048; RIBOSOMAL S6; 1.
Ribosomal protein; rRNA-binding; Complete proteome.
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
RPSF OR YPO3539 OR Y0645.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Perry Ř.D.;
"Genome sequence of Yersinia pestis KIM.";
J. Bacteriol. 184:4601-4611(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AP005082; BAC61003.1; -.
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les 5; Conservative
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SPECIES=E.coli; STRAIN=0157:H7 / RIMD 0509952;
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Q8XG88;
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RS6_SALTY
ID RS6_S
       RAPARA RA
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                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence
of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
SPECIES=E.coli; STRAIN=0157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551,
MEDLINE=21074935; PubMed=11206551,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Bouttin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
"Genome sequence of enterchaemorrhagic Escherichia coli 0157:H7.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=217992, 83334, 623;
                                     similarity).
-!- SIMILARITY: BELONGS TO THE S6P FAMILY OF RIBOSOMAL PROTEINS.
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Binds together with S18 to 16S ribosomal RNA (By
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAMAP, MF 00360; -; 1.
InterPro; IRR006529; Ribosomal S6.
Pfam, PF01250; Ribosomal S6; 1.
Prodom, PD003809; Ribosomal S6; 1.
TIGRFAMS; TIGR00166; S6; 1.
PROSITE; PS01048; RIBOSOMAL S6; 1.
Ribosomal protein; FRNA-binding; Complete proteome. SEQUENCE 130 AA; 15008 MW; 7897E436DD1FAS62 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
30S ribosomal protein S6.
30S ribosomal protein S6.
Escherichia coli 06,
Escherichia coli 06,
Escherichia coli 0157:H7, and
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54 LHKAHYVL 61
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Best Local Similarity
Matches 5; Conserv
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   FUNCTION:
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RS6 ECOL6
Q8XDI1;
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1897 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 1917 - 191
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0
MEDLINE=21156231, PubMed=11258796,
Haysahi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
Kuhara S., Shiba T., Hattori M., Shinagawa H.;
Complete genome sequence of enterohemorrhagic Escherichia coli
O157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-4441(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
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-!- SIMILARITY: BELONGS TO THE S6P FAMILY OF RIBOSOMAL PROTEINS.
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Prodom; PR0126) Ribosomal S6; 1
Prodom; PR01269; Ribosomal S6; 1.
TIGRFAMS; TIGR00166; S6; 1.
PROSITE; PS01048; RIBOSOMAL S6; 1.
Ribosomal protein; RRNA-binding; Complete proteome.
SEQUENCE 131 AA; 15187 MW; 01CIFD0EF4197ED2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
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EMBL; AE005652; AAG59396.1; -...
EMBL; AE005568; BAB38599.1; -...
EMBL; AE015442; AAN45771.1; -...
PIR; C65231; R3EC6.
PIR; H86116; H86116.
PIR; H91275; H912
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RPSF OR STM4391 OR STY4747 OR T4442.
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NCBI_TaxID=602, 601;
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nes 5; Conserv
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21-JUL-1986 (Rel. 01,
21-JUL-1986 (Rel. 01,
15-SEP-2003 (Rel. 42,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Deng W., Liou S.R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
and CT18.";
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                               PRECIESES typhimurium, STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES. S. typhi; STRAIN=CT18; SEQUENCE FROM N.A.
SPECIES. S. typhi; STRAIN=CT18; MEDIINE=2153494; PubMed=1167608; MEDIINE=2153494; PubMed=1167608; Parkhill J.; Dougan G., James K.D., Thomson N.R., Pickard D., Wain J. Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; Simmonds M., Skelton J., Stevens K., "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
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-!- SIMILARITY: BELONGS TO THE S6P FAMILY OF RIBOSOWAL PROTEINS.
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-!- FUNCTION: Binds together with S18 to 16S ribosomal RNA (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68.0%; Score 34; DB 1; Length 131; 62.5%; Pred. No. 9.2; cive 2; Mismatches 1; Indels
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ProDom; PD003809; Ribosomal_S6; 1.
TIGRPAMs; TIGRO166; S6; 1.
PROSITE; PS01048; RIBOSOMAL S6; 1.
Ribosomal protein; RRNA-binding; Complete proteome.
SEQUENCE 131 AA; 15173 MW; 54974D6342C21362 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPECIES=S.typh; STRAIN=Ty2 / ATCC 700931; MEDLINE=22531367; PubMed=12644504;
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EMBL, AL627283; CAD06868.1; -.
EMBL, AE016849; AAO71889.1; -.
SAGOROF, SG727?; TypsF.
HAMAP, MF 00360; -; 1.
InterPro; IPR000529; Ribosomal_S6.
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135 AA

PRT;

STANDARD;

RS6_ECOLI P02358;

RESULT 15 RS6 ECOLI ID RS6 E AC P0235

||| ||:: 54 LHKAHYVL 61 2 LHKVHYLV 9

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Hitz H., Schaefer D., Wittmann-Liebold B.;
"Determination of the complete amino-acid sequence of protein S6 from
"the wild-type and a mutant of Escherichia coli.";
Eur. J. Biochem. 75:497-512 (1977).
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                                                                                                                                                            SEQUENCE OF 1-131 FROM N.A.
MEDLINE-86310297; PubMed=3528756;
Schnier J., Kitakawa M., Isono K.;
"The nucleotide sequence of an Escherichia coli chromosomal region containing the genes for ribosomal proteins S6, S18, L9 and an open
                                                                                               Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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Wilkins M.R., Gasteiger E., Tonella L., Ou K., Tyler M.,
Sanchez J.-C., Gooley A.A., Walsh B.J., Bairoch A., Appel R.D.,
Williams K.L., Hochetrasser D.F.,
"Protein identification with N and C-terminal sequence tags in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MASS SPECTROMETRY.
STRAIN-K12 / ATCC 25404;
MEDLINE=99196679; Pubmed=10094780;
Arnold R.J., Reilly J.P.;
"Observation of Escherichia coli ribosomal proteins and their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pasquali C., Sanchez J.-C., Ravier F., Golaz O., Hughes G.J., Frutiger S., Paquet N., Wilkins M., Appel R.D., Bairoch A., Hochstrasser D.F.,
                                                                                                                                                                                                                                                                                                                                                                           "Analysis of the Escherichia coli genome VI: DNA sequence of region from 92.8 through 100 minutes.";
Nucleic Acids Res. 23:2105-2119(1995).
                                                                                                                                                                                                                                                                                                                             MEDLINE=95334362; PubMed=7610040;
Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       posttranslational modifications by mass spectrometry.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-99085675; PubMed-9868784; Wathinger V.C., Humpbry-Smith I.; Manlager V.C., Humpbry-Smith I.; Manlal genes/gene-products in Escherichia coli K-12."; FEMS Microbiol. Lett. 169:375-382(1998).
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   15-SEP-2003 (Rel. 01, Last sequence update) 308 ribosomal protein S6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Link A.J., Robison K., Church G.M.;
"Comparing the predicted and observed prop
in the genome of Escherichia coli K-12.";
Electrophoresis 18:1259-1313 (1997).
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MEDLINE=77225229; PubMed=328274;
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                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-131 FROM N.A. STRAIN=K12 / MG1655;
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STRAIN=K12 / W3110;
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STRAIN=K12 / EMG2;
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                                                                                 Escherichia coli
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                                                                                                                                 NCBI_TaxID=562;
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                                                                RPSF OR B4200
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This SWISS-FROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                    NAL. SERUCE, BIOL. 9:750-755 (2002).

-I. FUNCTION: BINDS TOGETHER WITH $18 TO 16S RIBOSOMAL RNA.

-I. FUNCTION: BINDS TOGETHER WITH $18 TO 16S RIBOSOMAL RNA.

-I. FUNCTION: BINDS TOGETHER WITH $18 TO 16S RIBOSOMAL RNA.

-I. FUNCTION: BINDS OF THE PORMS OF THE PROTEIN, VARYING ONLY IN THE NUMBER SEQUENCE SHOWN IS FORM $6-6, WHICH IS THE LONGEST. THE FIRST 2 GLU ARE ENCODED BY THE RAPE FORD, THE OTHER GLU ARE ADDED FOST-

TRANSLATIONALLY BY THE RIMK ENZYME.

-I. MASS SPECTROMETRY: WW-118187.2, METHOD-WALDI; RANGE=1-131.

-I. SIMILARITY: BELONGS TO THE $6P FAMILY OF RIBOSOMAL PROTEINS.
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Prodom; PD03809; Ribosomal_S6; 1.

TIGREAMS; TIGRO0166; S6; 1.

PROSITE; PS01048; RIBOSOMAL_S6; 1.

Ribosomal protein; rRNA-binding; 3D-structure; Complete proteome.

CHAIN 1 132 30S RIBOSOMAL PROTEIN S6, NON-MODIFIED ISOPORM.

CHAIN 1 135 30S RIBOSOMAL PROTEIN S6, FULLY MODIFIED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                  Tung C.-8., Joseph S., Sanbonmatsu K.Y.; "All-atom homology model of the Escherichia coli 30S ribosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 68.0%; Score 34; DB 1; Length 135; Best Local Similarity 62.5%; Pred. No. 9.5; Matches 5; Conservative 2; Mismatches 1; Indels
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G -> A (IN REF. 4).
F4CC629711C1FDOE CRC64;
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EMBL; U14003; AAA97096.1; --
EMBL; AE000491; AAC7157.1; --
PDB; 1MSC; 09-JUL-02.
SWISS-2DPAGE; P02358; COLT.
ECC2DBASE; OD14.7; ETH EDITION.
ECC2DBASE; CO14.8; ETH EDITION.
ECC2DBASE; CO14.8; ETH EDITION.
ECC2DBASE; CO15.3; ETH EDITION.
ECC2DBASE; CO15.3; ETH EDITION.
ECC3CBASE; CO15.3; ETH EDITION.
ECC3CBASE; CO15.3; ETH EDITION.
INTERPRO; IPPRO00529; RIDOSOMAI_SC.
                                                                                                                         MEDLINE=22239879; PubMed=12244297;
Anal. Biochem. 269:105-112(1999).
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135 AA; 15703 MW;
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Search completed: December 16, 2003, 14:15:16 Job time : 6.66667 secs 54 LHKAHYVL 61

2 LHKVHYLV 9

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Run

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Q8rvy8 brassica ca
Q8s9c1 brassica ca
Q8s9c1 brassica ca
Q8rvy9 brassica ca
Q8rdy staphylococ
Q8tdj7 homo sapien
O9tty4 canis famil
Q9tty4 canis famil
Q8tdj8 homo sapien
O423p2 rickettsia
Q82gp2 rickettsia
Q8tdj9 homo sapien
Q81dy9 homo sapien
Q81dy9 homo sapien
Q81dy1 homo sapien
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Ogcwl2 mus musculu
Ogwq17 homo sapien
Ogy977 aeropyrum p
Og870y4 salmonella
Ogn798 homo sapien
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Q8r9b9 thermoanaer
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28i077 drosophila
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio,
NCBI_TaxID=7955;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adams J.C., Zaromytidou A.-I.;
"Zebrafish muskelin from cDNA ";
"Zebrafish muskelin from cDNA ";
Submitted (SEP-2001) co.the EMBL/GenBank/DDBJ databases.
EMBL; AF418017, AANJ266411;
SEQUENCE 729 AA; 84376 MW; DFB3672F5D0AE16F CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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                                   Q8S9C2
Q8RVY8
Q8S9C1
Q8RVZ0
Q8RVY9
Q8CND4
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Q92GP2
Q8TDJ9
Q8NGZ7
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092HR4
08DCL6
08EAH2
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Q8R9B9
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Q9CWL2
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Q9Y977
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Q8N798
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01-JUN-2002 (TrEMBLrel. 21, C
01-JUN-2002 (TrEMBLrel. 21, L
01-MAR-2003 (TrEMBLrel. 23, L
Chitin synthase V.
CHS5.
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Matches 7; Conservative
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Muskelin,
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Q8AYJ5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 2
Q8TGV2
ID Q8TG
AC Q8TG
DT 01-J
DT 01-M
DE Chit
GN CHSS
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8tgy2 exophiala d 99gkx9 sus scrofa 09gkx9 sus scrofa 077563 aus scrofa 08tx44 mus musculu Q8xkm8 flostridium 094k11 arabidopsis 08k4f0 mus musculu 02327 arabidopsis 092c5 listeria in 08y7x7 listeria in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8ayj5 brachydanio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                      2003, 14:09:45; Search time 25 Seconds (without alignments) 92.899 Million cell updates/sec
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           5.1.6
Compugen Ltd.
                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                          830525 seqs, 258052604 residues
           GenCore version (c) 1993 - 2003
                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                              using sw model
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Q8K4F0
O23227
Q92CR5
Q8Y7X7
Q92CM1
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Q8TGV2
Q9GKX9
O77563
Q8T2D3
Q8K4E4
                                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
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Q960B2
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sp_bacteria:*
sp_fungi:*
sp_fungi:*
sp_human:*
sp_mammal:*
sp_mc:*
sp_mc:*
sp_phage:*
sp_phage:*
sp_phage:*
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sp_vertebrate:*
sp_unclassified:*
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sp_bacteriap:*
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50
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Maximum DB seq length: 200000000
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                                                                                         December 16,
                        Copyright
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648444
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GTRAIN-AX4;
Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,
Gloeckner G., Eichinger L., Szafranski K., Guigo R., Kumpf K.,
Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
Sequence and Analysis of Chromosome 2 of Dictyostelium.";
Sequence and Analysis of Chromosome 2 of Dictyostelium.";
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AC115613; AANIO762.!
InterPro: IPR003006; Ig MHC.
InterPro: IPR000648; Oxysterol_BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBL_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74.0%; Score 37; DB 6; Length 364; 77.8%; Pred. No. 53; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74.0%; Score 37; DB 5; Length 439; 55.6%; Pred. No. 64;
                                                                                                                                                                                                                                                                                                                                                   Meljerink B., Voegeli P., Stranzinger G.;
Meljerink B., Voegeli P., Stranzinger G.;
"The putative porcine blood group A transferase cDNA.";
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AFCS0177; AACG8840.1;
INTERPRO; IPRO05076; Glyco_trans_6.
Pfam; PF03414; Glyco_transf_6; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       al protein.
439 Aa; 49590 MW; 65F0C94E40E4AAD9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   364 AA; 42258 MW; 3D51850110EE75EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dictyostellum discoideum (Slime mold).
Eukaryota, Mycetozoa, Dictyostellida, Dictyostellum.
NCBI_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8T2D3 PRELIMINARY; PRT; 439 AA.
Q8T2D3;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 49.6 kDa protein.
                        01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               187 AA
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                                                                                                                   Putative blood group A transferase
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PROSITE; PS00290; IG MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel, 22, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 77.8%; nes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 55.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          380 FIHKPHYFI 388
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                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                 Sus scrofa (Pig)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical
SEQUENCE 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transferase.
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Q8K4E4
ID Q8K4I
AC Q8K4I
DT 01-00
DT 01-00
DT 01-00
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                                                                                                                                               SEQUENCE FROM N.A.

A Liu H., Szaniszlo P.J.;

RT "Cloning and Characterization of a class V Chitin Synthase Gene
Liu H., Szaniszlo P.J.;

RT (WCHESS) of Wangiella (Exophiala) dermatitidis, A Model Dematiaceous

RT Pathogen of Humans.";

RT Pathogen of Humans.";

RT Pathogen of Humans.";

RT PATHOGEN OF HAL19810.1;

DR REPEPPO; IPR001199; Cyt. BS.

DR InterPro; IPR001169; Wyosin head.

DR InterPro; IPR00169; Wyosin head.

DR Pfam; PF00173; heme 1; 2.

DR Pfam; PF00063; Wyosin head; 1.

DR Pfam; PF00055; CYTOCHROWE BS. 2; 1.
                            Eukāryota; Fungi; Ascomycotā; Pezizomycotina; Chaetothyriomycetes;
Chaetothyriales; Herpotrichiellaceae; mitosporic Herpotrichiellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Mammalian ABO genes: Murine AB gene encodes a glycosyltransferase with both A and B transferase activity and porcine O gene is a null allele due to a major chromosomal aberration.", Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, ABO41040, BABZ0561.1;

InterPro, IPR005076; Glyco trans 6.

Pfam; PF03414; Glyco trans 6.

Transferase.

NON TER

152 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78.0%; Score 39; DB 3; Length 188
85.7%; Pred. No. 1.1e+02;
ative 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
A transferase (Fragment).
   Exophiala dermatitidis (Wangiella dermatitidis)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     364 AA.
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1; Mismatches
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Mammalia; Eutheria;
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FLHEVDYLV
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Best Local Similarity
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                                                                                                                      NCBI_TaxID=5970;
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Matches

RESULT 3 Q9GKX9

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1; Mismatches
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                Score 36;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72.0%; Score 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interpro; IPR000073; A/b hydrolase.
Interpro; IPR003089; AB hydrolase.
Interpro; IPR000639; Bpox hydrolase.
Interpro; IPR000379; Ser_estrs_site.
Pfam; PF00561; Abhydrolase; 1.
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01-0CT-2002 (TrEMBLrel. 22, Last seq
01-MAR-2003 (TrEMBLrel. 23, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00111; ABHYDROLASE.
PRINTS; PR00412; EPOXHYDRLASE.
                72.0%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71.48;
           Query Match
Best Local Similarity 75.0
Matches 6; Conservative
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Matches 5; Conservative
                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                  22 LHYVHYLI 29
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Q8K4F0
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                                                                                                                                                                                                                                                         "Tissal (PTA) activation antigen implicated in T cell differentiation and platelet activation is a member of the immunoglobulin superfamily exhibiting distinctive regulation of expression."; J. Biol. Chem. 272:21735-21744 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jin B., Zhang X., Li D., Ouyang W., Jia W., Chen L., Xie X., Ning S., Zhang Y.; "Gene cloning and characterization of mouse platelet and T cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shimizu I., Ohtani K., Hirakawa H., Ohshima K., Yamashita A., Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.; Complete genome sequence of Clostridium perfringens, an anaerobic flesh-eater.";

Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).

BRBL; APO03190; BAB8072.1;

Hypothetical protein; Complete proteome.

SEQUENCE 250 AA; 29634 MW; 60F81BD7DFD6C973 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=BALB/C;
MEDLINE=20112343; PubMed=10647817;
MEDLINE=20112343; PubMed=10647817;
Aia H., Liu D., Xia H., Liu X., Jia W., Sun C., Sun K., Jin B.;
"Isolation of cDNAs encoding gibbon and monkey platelet and T cell activation antigen 1 (PTA1).";
DNA Seq. 10:155-161(1999).
                    Mus musculus (Mouse).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butharia; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clostridium perfringens.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
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                                                                                                                                                STRAIN=BALB/C;
MEDLINE=97413766; PubMed=9268302;
MEDLINE=97413766; PubMed=9268302;
Sherrington P.D., Scott J.L., Jin B., Simmons D., Dorahy S.J.,
Lloyd J., Brien J.H., Aebersold R.H., Adamson J., Zuzel M.,
Burns G.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 36; DB 11; Length 187;
Pred. No. 43;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                activation antigen I (PTA1/CD226).";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, 74f21198; AAN04296.1;
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
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PROSITE; PS50835; IG LIKE; 1.
SEQUENCE 187 AA; 21393 MW; 70D29BE21927ACE5 CRC64;
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1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein CPE1366.
Platelet and T cell activation antigen 1 isoform 1.
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62.5%;
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Best Local Similarity
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                                                                                      NCBI_TaxID=10090;
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NCBI_TaxID=1502;
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PubMed=11792842;
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Lam B. Southwick A., Karlin-Neumann G., Nguyen M., Miranda M., Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H., Cheuk R., Chung M.K., Haysehizaki Y., Ishida J., Kamiya A., Kawai J., Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H., Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K., Bcker J., Theologis A., Davis R.W.;

Ecker J., Theologis A., Davis R.W.;

Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.

I- FUNCTION: BIOTRANSFORMATION ENZYME THAT CATALYZES THE HYDROLYSIS
OF EPOXIDES (ALKENE OXIDES, OXIRANES) AND ARENE OXIDES TO LESS
REACTIVE AND MORE WATER SOLUBLE DIHYDRODIOLS BY THE TRANS ADDITION
OF WATER (BY SIMILARITY: AN EPOXIDE + H(2)O = A GLYCOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
UNAR-2003 (TrEMBLrel. 23, Beoxide hydrolase).
Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-BALB/c; IISSUE=Thymus;
Jin B., Zhang X., Li D., Ouyang W., Jia W., Chen L., Xie X., Ning S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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SEQUENCE 321 AA; 35777 MW; C1031E942DDD5F34 CRC64;
DB 16; Length 250;
57;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                  321 AA.
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2; Mismatches
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Hypothetical protein; Aromatic hydrocarbons catabolism;
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Q92CR5
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-2003 (TrEMBLrel. 23, Last annotation update)
Hypochetical protein (EC 3.3.2.3) (Epoxide hydrolase).
C7A10.830 OR AT4G36530.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
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                                                                                                                                                                                                                                                                                                                                                                                          Score 36; DB 11; Length 333;
Pred. No. 75;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bevan M., Terryn N., Vos P., Heijnen L., Mewes H.W., Sch
Chalwatzis N.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                         Pfam; PF00047; ig; 2.
SMART; SM00409; IG; 2.
PROSITE; PS50835; IG_LIKE; 2.
SEQUENCE 333 AA; 38063 MW; ACDE524D0F475C97 CRC64;
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EMBL, AV087588, AAM55130.1; -...
EMBL, AV087588, AAM55130.1; -...
InterPro; IPR000073, AP, bydrolase.
InterPro; IPR000639; Box_hydrolase.
InterPro; IPR000379; Ser_estrs_site.
Pfam, PF00561; abhydrolase; I...
PRINTS; PR00111; ABHYDROLASE.
PRINTS; PR00111; ABHYDROLASE.
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Query Match
Best Local Similarity 62.5%,
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Genome Biol. 0:0-0(2002).
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76 YLHRVHFL 83
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NCBL TaxID=3702;
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                                                                                                      Score 36; DB 10; Length 378;
Pred. No. 85;
2; Mismatches 0; Indels
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 21, Last annotation update)
101-MIN-2002 (TrEMBLrel. 21, Last annotation update)
1001142.
11. Steria monocytogenes.
11. Steria monocytogenes.
12. Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
NCBI_TAXID=1639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
NCBL_TaxID=1642;
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Listilist, LIN01106; -.
Listilist, LIN01106; -.
LinterPro; IPR001450; 4P64S. ferredoxin.
InterPro; IPR001495; Complex1.51K.
Pfam; PF01512; Complex1.51K; I.
Pfam; PF00037; fer4; 1.
PROSITE; PS00198; 4F642; ERRREDOXIN; 1.
Hypochetical protein; Complete proteome.
SEQUENCE 454 AA; 49918 MW; 068B138B9213B239 CRC64;
Decoxification, Hydrolase.
SEQUENCE 378 AA, 41906 MW; 8DIFB39D5410E818 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein lin1106.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             454 AA
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STRAIN=CLIP 11262 / Serovar 6a;
                                                                                                              72.0%;
                                                                                                                                                       71.48;
                                                                         Query Match
Best Local Similarity 71.4%,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 71.4 tes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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239 YLHKLHY 245
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89 HKIHYVV 95
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01-MAR-2003 (TrEMBLrel. 23, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Conservative
                                                                                        PRELIMINARY;
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526 FQHRIHYL 533
                      500 LHNVHYLL 507
 2 LHKVHYLV 9
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Matches 5: Conserv
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                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                      NCBI TaxID=36329;
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                                                             RESULT 14
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                                            Character P., Frangeul L., Buchrieser C., Rusnick C., Amend A.,

Adlaser P., Frangeul L., Buchrieser E., de Darnvar A., Dehoux P.,

Adrabit A., Chetouani F., Couve B., de Darnvar A., Dehoux P.,

Domann E., Dominquez-Bernal G., Duchaud E., Durant L., Dussurget O.,

Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,

Adulier L., Goobel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,

Jones L.-M., Kaerst U., Kaerst U., Krust F., Kurnskt G.,

Madueno E., Maitournam A., Mata Vicente J., Ng B., Nedjari H.,

Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

Remmel B., Rose M., Schlueter T., Simces N., Tierrez A.,

Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;

Comparative genomics of Listeria species.";

EMBI, AL591978; CAC99220.1;

Listinist; LM001142;

Listinist; LM001142;

Listinist; LM001142;

Listinist; LM001142;

Rems, PF01512; Complex1 51K.

Pram; PF01512; Complex1 51K.

Pram; PF01512; Complex1 51K.

PROSITE; PS00198; 4FE4S FERREDOXIN; 1.

SEQUENCE 454 AA, 49891 MW; 006AD6F5C732B44B CRC64;
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MEDLINE=9903489; PubMed=9823893;
MEDLINE=9039489; Zomorodipour A., Andersson J.O.,
Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
Eriksson A.-S., Winkler H.H., Kurland C.G.;
"The genome sequence of Rickettsia prowazekii and the origin of
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Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                         Score 36; DB 16; Length 454;
Pred. No. 1e+02;
2: Mismatches 0; Indels
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75.0%; Pred. No. 1.5e+02;
tive 1; Mismatches 1; Indels
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(1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAX-2003 (TrEMBLrel. 23, Last annotation update)
Cytochrome C-type biogenesis protein CCMF (CCMF).
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EMBL, AJ235273; CAA15139.1; -.

InterPro; IPR002541; Cytc asm.

InterPro; IPR0002567; Cyt c biog.

InterPro; IPR000276; GPGRRADS.

PEAM; PF01578; Cytc asm; I.

PRINTS; PR01410; CCBIOGENESIS.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

Complete protecome.

SEQUENCE 670 AA; 76847 MW; 2703AlAC44F9EB
                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=EGD-e / Serovar 1/2a;
MEDLINE=21537279; PubMed=11679669;
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Best Local Similarity 75.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rickettsia prowazekii.
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239 YLHKLHY 245
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Gardner M.J., Hall N., Fung B., White O., Berriman M., Hyman R.W., Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K., Bisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S., Chan M.-S., Nene V., Shallon S.J., Suh B., Peterson J., Angiuoli S., Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B., Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A., McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C., Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
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MEDLINE-20195006; PubMed=10731132;
Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
Ananatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
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Bukaryota, Metazoa, Arthropoda, Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                             Přio 0290.
Plasmodium falciparum (isolate 3D7).
Eukaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72.0%; Score 36; DB 5; Length 702; 62.5%; Pred. No. 1.6e+02; ive 2; Mismatches 1; Indels
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Hypothetical protein.
SEQUENCE 702 AA; 82907 MW; 37D1DDB57A12AE6B CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
CG8202 protein.
                                                                                                                              01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
702 AA.
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Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Charlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cabley S., Dallke C., Davenport L.B., Davies P., de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Bablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Duckon K., Doup L.E., Downee M., Dugan-Rocha S., Pleischmann W., Rabubin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Rabuch F., Gong F., Gorgel S., Galbart W.M., Glasser K., Gadzielian A.E., Garg N.S., Gelbart W.M., Glasser K., Radode R., Goriell J.H., Gu Z., Kennison J.R., Houck J., Balali M., Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegama C., Jank Hostnin D., Kalueh F., Karpen G.H., Ke Z., Kennison J.R., McChum K.A., Jalali M., Kalueh F., Karpen G.H., Ke Z., Kennison J.R., Laiz Z., Linn X., Jalali M., Malush F., Karpen G.H., Ke Z., Kennison J.R., Laiz Z., Linn X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.L., RA McHulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Nelson D.R., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Rak Shue B.C., Siden Kiamos I., Simpson M., Strong R., Sun H., Stee R., Spradling A.C., Stapleron M., Strong R., Sun B., Svirskas R., Tector C., Turner R., Venter E., Wang S., Yao Q., Zhong X., Walliams S.M., Woodage T., Worlect D.C., Zhu R., Walliams S.M., Woodage T., Worley K.C., Shu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; Zhu X., Shu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; Shu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; Shu S., Zhu X., Smith H.O., Sunce 287:2185-2195 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Celniker S. B., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
A Banzon J., Adams M.D., Amanatides P.G., Brandon R.C., Rogers Y.,
Banzon J., An H., Baldwin D., Banzon J., Beeson K.C., Rogers Y.,
Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
A Carlson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
A Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Numoo J.,
A pacleb J., Paragas V., Park S., Patel S., Pfeiffer B., Scheeler F.,
Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
A Williams S.M., Zaveri J.S., Puni H.O., Venter J.C., Rubin G.M.,
Sequencing of Drosophila melanogaster genome.",
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.B., Smith C.D., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.B., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.B., Clamp M., Drysdale R., Emmert D., Frise B., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith B., Shu S., Smutniak F., Whitfield B., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.; "Annotation of Drosophila melanogaster genome."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J., Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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FlyBase; FBgn0037622; CG8202.
SEQUENCE 716 AA; 82149 MW; 4DB233CE393C5704 CRC64;
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Best Local Similarity 71.*.
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Gaps

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72.0%; Score 36; DB 5; Length 716; 71.4%; Pred. No. 1.6e+02; ative 2; Mismatches 0; Indels

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622 FIHKVHF 628
1 FLHKVHY 7
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completed: December 16, 2003, 14:18:03 Job time : 27 secs Search

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Query Match
Best Local Similarity 77.8
Matches 7; Conservative
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STRANDEDNESS: single
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
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TOPOLOGY:
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RESULT 1
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Sequence 1, Appli
Sequence 10, Appli
Sequence 5331, Ap
Sequence 2, Appli
Sequence 2, Appli
Sequence 15, Appli
Sequence 15, Appli
Sequence 15, Appli
Sequence 15, Appli
Sequence 25132, A
Sequence 6483, Ap
Sequence 6483, Ap
Sequence 6483, Ap
Sequence 6483, Ap
Sequence 611, Appl
Sequence 611, Appl
Sequence 21, Appl
Sequence 614, Appl
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Appli
Appli
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                                                       December 16, 2003, 14:11:00 ; Search time 12.3333 Seconds (without alignments) 30.875 Million cell updates/sec
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Sequence
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2: /cgn2 6/ptodata/1/iaa/5B COMB.pep:*
3: /cgn2 6/ptodata/1/iaa/6A COMB.pep:*
4: /cgn2 6/ptodata/1/iaa/6B COMB.pep:*
5: /cgn2 6/ptodata/1/iaa/PCTUS COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep:*
        GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-425-678-10
US-09-107-52A-5331
US-08-107-52A-5331
US-08-258-614-2
US-08-828-56-2
US-09-360-197-6
US-09-636-077A-15
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US-09-328-355-6483
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US-08-868-458-2
US-09-252-991A-30355
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                                                                                                                                                                          Total number of hits satisfying chosen parameters:
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                                                                                                                                                          328717 seqs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                          OM protein - protein search, using sw model
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Maximum DB seq length: 2000000000
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S5
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                                                                                                               1 KHFKPHGFS 9
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                                                                                                                                 BLOSUM62
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31, Appl
6, Appli
6035, Ap
20, Appl
77, Appl
20307, A
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26757, A
19630, A
18540, A
26961, A
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APPLICANT: Flores, Maria V
APPLICANT: Flores, Maria V
APPLICANT: Flores, Maria V
APPLICANT: O'Sullivan, William J
TITLE OF INVENTION: Phosphate synthetase II
TITLE OF INVENTION: phosphate synthetase II
NUMBER O'SEQUENCES:
ADDRESSE: Nixon & Vanderhye PC
STREET: 1100 No. 5849573th Glebe Road, 8th Floor
CITY: Arlington
STATE: Virginia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
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US-09-732-210-480
US-09-732-210-1179
US-09-732-210-1179
US-08-157-005-6
US-08-799-464A-20
US-08-799-464A-20
US-08-79-863-6
US-08-79-863-6
US-09-019-793A-31
US-09-155-864-6
US-09-155-9035-0035
PCT-USS5-10904-77
US-09-152-991A-20307
US-09-107-532A-5293
US-09-107-532A-2293
US-09-252-991A-18540
US-09-252-991A-18540
US-09-252-991A-18540
US-09-252-991A-18540
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COMPUTER, IBM PC compatible
COMPUTER, IBM PC compatible
COMPUTER, IBM PC compatible
SOFTWARE: PatentIn Release #1.24
APPLICATION NUMBER: US/08/446,855A
FILING DATE: 06-01-1995
CLASSIFICATION: 435
ATTORNEY,PAGENT INFORMATION:
NAME: Mitchard, Leonard C
REGISTRATION NUMBER: 29.009
REFERENCE/DOCKET NUMBER: 29.009
REFERENCE/DOCKET NUMBER: 47-80
TELECHONE: 703-816-4100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2391 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08446855A Patent No. 5849573 GENERAL INFORMATION:
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Sequence 10, Application US/09425679E
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                                                                                  Sequence 2, Application US/09150741

Patent No. 618396

GENERAL INFORMATION:

APPLICANT: Stewart et al.

TITLE OF INVENTION: Nucleotide Sequence Encoding Carbamoyl Phosphate
Patent No. 6183996

PATENTE OF INVENTION: Synthetase II

FILE REFERENCE:

CURRENT PILING DATE: 1998-09-10

EARLIER APPLICATION NUMBER: US/09/150,741

CURRENT FILING DATE: 1998-10-10

EARLIER APPLICATION NUMBER: P16380

EARLIER APPLICATION NUMBER: 08/46,855

EARLIER PILING DATE: 1993-12-16

EARLIER PILING DATE: 1993-12-06

EARLIER PILING DATE: 1993-12-06

SARLIER PILING DATE: 1995-07-06

NUMBER OF SEQ ID NOS: 15

SEQ ID NO 2

LENGTH: 2391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: McDonald, Thomas L.
APPLICANT: McDonald, Thomas L.
TITLE OF INVENTION: Serium Amyloid A Isoform from Colostrum
FILE REFERENCE: UNMC 61142
CURRENT APPLICATION NUMBER: US/09/425,679E
CURRENT FILING DATE: 1999-10-22
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 60/218,611
PRIOR FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.1
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 74.5%; Score 41; DB 3; Length 2391; Best Local Similarity 77.8%; Pred. No. 39; Matches 7; Conservative 1; Mismatches 1; Indels
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US-09-425-679E-8
'Sequence 8, Application US/09425679E
'Patent No. 6509444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT; ORGANISM: Equus caballus
US-09-425-679E-8
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7 HFRPHG 12
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                                               RESULT 2
US-09-150-741-2
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US-09-425-679E-10

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APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               o'
Patent No. 6509440

GRANEAL INFORMATION:
APPLICANT: Weber, Annika L.
APPLICANT: Weber, Annika L.
TITLE OF INVENTION: Serum Amyloid A Isoform from Colostrum
FILE REPERENCE: USANG 63142
CURRENT PILION NUMBER: US/09/425,679E
CURRENT PILION DATE: 1999-10-22
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-14
PRIOR PILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.1
SEQ ID NO 10
LENGTH: 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 67.3%; Score 37; DB 4; Length 110; Best Local Similarity 83.3%; Pred. No. 7.5; Matches 5; Conservative 1; Mismatches 0; Indels
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CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 MAY 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5331, Application US/09107532A Patent No. 6583275 GENERAL INFORMATION:
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LENGTH: 508 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (781)893-8277
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COUNTRY: USA
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MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Equus caballus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Waltham
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Sequence 2, Application US/08258614
Patent No. 5432070
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Patent No. 5213969
GENERAL INPORMATION:
APPLICANT: SCHUMACHER, Gunther
APPLICANT: BURTSCHER, Helmut
APPLICANT: MOLLERING, Hans
TITLE OF INVENTION: CLONED N-METHYLHYDANTOINASE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Armstrong, Nikaido, Marmelstein, Kubovcik & ADDRESSEE: Marminay
STREET: 1725 K Street, N.W., Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1288;
                                                                                                                                                    Score 37; DB 4; Length 508;
Pred. No. 39;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Washington D.C.
COUNTRY: United States of America
ZIP: 2006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/727,814B
FILING DATE: 19910708
CLASSIFICATION: 435
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Pred. No. 1.1e+02;
                                 , NAME/KEY: misc_feature; LOCATION: (B) LOCATION 1...508; SEQUENCE DESCRIPTION: SEQ ID NO: 5331: US-09-107-532A-5331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
 ORIGINAL SOURCE: ORIGINAL SOURCE: ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 4021571.7
FILING DATE: 06-JUL-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Murray, Robert B.
REGISTRATION NUMBER: 22,980
REFERENCE/DOCKET NUMBER: 9110
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 659-2930
TELEPHONE: (202) 887-0357-
                                                                                                                                                    Query Match
Best Local Similarity 85.7%;
Matches 6; Conservative C
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66.7%;
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1288 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: protein US-07-727-814B-2
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97 RHKKPHNFS 105
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US-07-727-814B-2
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US-08-258-614-2
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Sequence 2, Application US/08828596
Patent No. 5822018
GENERAL INFORMATION:
APPLICANT: Welsh, Michael J.
APPLICANT: Welsh, Michael J.
APPLICANT: Price, Magaret P.
TITLE OF INVENTION: and DNA Sequences Encoding Same
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zarley, McKee, Thomte, Voorhees & Sease
STREET: 801 Grand Suite 3200
CITY: Des Moines
STATE: Lowa
COUNTRY: United States
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                                                                                                                                                                                           ADDRESSEE: Nikaido, Marmelstein, Murray & Oram
STREET: 655 Fifteenth Street N.W. Suite 330
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/258,614
GENERAL INFORMATION:
APPLICANT: SCHUMACHER, Gunther
APPLICANT: BURTSCHER, Helmut
APPLICANT: MOLLERING, Hans
TITLE OF INVENTION: CLONED N-METHYLHYDANTOINASE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
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PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/021,856
FILING DATE: 24-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 40 21 571.7
FILING DATE: 06-JUL-1990
PRIOR APPLICATION NUMBER: US/07/727,814
APPLICATION NUMBER: US/07/727,814
ATTORNEY, AGENT INFORMATION:
NAME: Kitts, MONIGE C.
REGISTRATION NUMBER: 36,105
REGISTRATION NUMBER: 36,105
REGISTRATION NUMBER: 36,105
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                     STATE: D.C.
COUNTRY: U.S.A.
ZIP. 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOSPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 67.3
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: protein US-08-258-614-2
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97 RHKKPHNFS 105
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TOPOLOGY: linear
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Best Local Similarity
Matches 5; Conserv
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US-09-635-872A-15
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APPLICANT: Basslana, Frederic
APPLICANT: Lazdunski, Michel
APPLICANT: Lazdunski, Michel
APPLICANT: Lazdunski, Michel
APPLICANT: Waldmann, Rainer
APPLICANT: Waldmann, Rainer
TITLE OF INVENTION: Human and Rat Families of Neuronal Acid-Sensitive
TITLE OF INVENTION: Cationic Channels, Their Cloning and Applications
TITLE OF INVENTION: Cationic Channels, Their Cloning and Applications
FILE REFERENCE: 989.6706P
CURRENT PELLING DATE: 1999.08/129, 758
PRIOR APPLICATION NUMBER: 09/129, 758
PRIOR APPLICATION NUMBER: 60/095,408
PRIOR APPLICATION NUMBER: 60/095,408
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIN Ver. 2.1
SEQ ID NO 6
LEAST SEQ ID NO 6
LEAST SEQ ID NO 6
LEAST SEQ ID NOS: 22
LEAST SEQ ID NO 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 35; DB 2; Length 512; Pred. No. 93;
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                                                   COMPUTER KEALABLE FORM:

COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BATERI PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,596
FILING DATE:
CLASSIFICATION NUMBER: US/08/826,838
FILING DATE: 02-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mebel, Heidi S.
REGISTRATION NUMBER: 37,719
REFERENCE/POCKET NUMBER: uirf n6-53
TELECOMMUNICATION INFORMATION:
TELEPHONE: 515-288-3667
TELEPHONE: 515-288-1338
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
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66.7%;
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amino acid
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                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            144 KHYKPKQFS 152
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KHFKPHGFS 9
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 6; Conserv
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RESULT 10

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Sequence 15, Application US/09635872A

Patent No. 6534300

GENERAL INFORMATION:
HILLIAM

TITLE OF INVENTION: METHODS FOR PRODUCING HIGHLY PHOSPHORYLATED LYSOSOWAL HYDROLASES
FILE REPERENCE: 195613US0

CURRENT APPLICATION NUMBER: US/09/635,872A

CURRENT APPLICATION NUMBER: 60/153,831

PRIOR FILING DATE: 1999-09-14

NUMBER OF SEQ ID NOS: 52

SOFTWARE: PatentIn version 3.0

SEQ ID NO 15

LENGTH: 908
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Fatent No. 6551795
GENERAL INFORMATION:
APPLICANT: MARCI O. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS:
TITLE OF INVENTION: AERCHGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT FILING DATE: 1999-02-18
FRIOR FILING DATE: 1999-02-18
FRIOR FILING DATE: 1998-02-18
FRIOR FILING DATE: 1998-02-18
FRIOR RILING DATE: 1998-02-18
FRIOR RILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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GENERAL INFORMATION:
GENERAL APPLICANT: CANFIELD, WILLIAM
APPLICANT: CANFIELD, WILLIAM
TITLE OF INVENTION: METHODS OF TREATING LYSOSOWAL STORAGE DISEASE
FILE REFERENCE: 195612US0
CURRENT APPLICATION NUMBER: US/09/636,077A
CURRENT FILING DATE: 2000-08-10
PRIOR PILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 52
SOFTWARE: Patentin version 3.0
SEQ ID NO 15
LENGTH: 908
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 63.6
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | :||||:
771 HRRPHGFA 778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Mus musculus
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Sequence 6483, Application US/09328352

Sequence 6483, Application US/09328352

Patent No. 6562958

GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

TITLE OF INVENTION: NUMBER: US/09/328,352

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 6483

LENGTH: 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 34; DB 4; Length 462;
Pred. No. 1.3e+02;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6483
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 85.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   202 FFPHGFS 208
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374 HFKPH 378
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US-09-328-352-6483
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US-09-252-991A-25132

US-09-252-991A-25132

Sequence 25132, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERABEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT PILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 363

LENGTH: 363
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                                                                                                                    Query Match 61.8%; Score 34; DB 4; Length 256; Best Local Similarity 71.4%; Pred. No. 67; Matches 5; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61.8%; Score 34; DB 4; Length 363; 100.0%; Pred. No. 98; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       h Similarity 100.0%; Pred. No. 1.1e+02; 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JAPPLICANT: Allen, Steve
APPLICANT: Allen, Steve
APPLICANT: Lee, Jian Ming
TITLE OF INVENTION: Plant Protein Kinases
FILE REFERENCE: BB-1171
CURRENT APPLICATION NUMBER: US/09/347,801
CURRENT FILING DATE: 1999-07-02
EARLIER FILING DATE: J199, 10, 1998
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Microsoft Office 97
SOFTWARE: Microsoft Office 97
LENGTH: 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20, Application US/09347801; Patent No. 6262345; GENERAL INFORMATION:
                                      TYPE: PRT / OKGANISM: Pseudomonas aeruginosa US-09-252-991A-19828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 61.8
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                         113 QHVKPHG 119
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Best Local Similarity
Matches 5; Conserv
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SEQ ID NO 19828
LENGTH: 256
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US-09-347-801-20
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beta-xylosidase [i
glycosyl hydrolase
probable beta-N-ac
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                                                               2003, 14:10:15; Search time 10.3333 Seconds (without alignments)
83.760 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                        283308 segs, 96168682 residues
                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                           OM protein - protein search, using sw model
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G88839
S45524
A28573
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H81913
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A71857
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AD0095
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Maximum DB seq length: 2000000000
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Match Length DB
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642
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754
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1: pir1:*
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Perfect score:
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hypothetical prote splicing factor RS splicing factor RS aspartate-B-semial splicing factor At spothetical prote hypothetical prote RepC2 replication sulfur oxidation phypothetical prote mRNA guanylyltrans 50S ribosomal prot	Father A (AMP.A), maxpbbb7, brancariorion f	02-Jun-2 den, J.M.	Reference number: A45377; MUID:92279218; PMID:1534408 Accession: A45377 Status: preliminary Molecule type: mRNA Residues: 1-351 < KRN> Cross-references: GB:M66842; NID:g181040; PIDN:AAA52071.1; PID:g181041 Fullimoto, A.; Nyunoya, H.; Morita, T.; Sato, T.; Shomotohno, K.		FIDN:BARA4234.1; FID:9220088 . an extensive family of leucine zipper pro MID:2516827	ot compared with conceptual translation 'R',330,'K',332-337,'L',339-341 <ha4> r</ha4>	DB 2; Length 351; 0.016; hes 0; Indels 0; Gaps 0;
110404 1471304 1471304 1471304 188294 108294 108797 108797 119579 119579 119579 119579 11957 119		vision 06-Ja 223 Huggenvik, J , 4820-4824, man CREB-2:	:92279218; P ID:9181040; rita, T.; Sa	NA binding p:91140735; Pd from GB/EM	ID:922008/; ; Green, M.R.R. CDNA clone:90185187; P.	Guence not shown; not 85-289,'R',291-328,'R TAXREB67; CREB-2 23551 transcription factor	Score 55; D; Pred. No. 0.
000000000000000000	human	7 Te	OID ,	r DJ GID ate	AT AT	89, 89, 1 .1	
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шшшшшшшшшч4444 Очиш45500000000000000000000000000000000000	RESULT 1 845377 transcription	C;Species: Homo sapiens (man) C;Date: 06-Jan-1995 #sequence C;Accession: A45377; 156787; DR;Karpinski, B.A.; Morle, G.D. Proc. Natl., Acad. Sci. U.S.A. A;Title: Molecular cloning of	A, Referer A, Accessi A, Status: A, Molecul A, Residue A, Cross-r R, Tsujimo	J. Virol. A,Title: A,Referen A,Accessi A,Status: A,Status: A,Residue	A, CLOSS - I R, Hai, T. Genes Dev A, Title: A, Referen A, Accessi	A.Status: nucleic acid sequence not sh A.Molecule type: mRNA A.Residues: 274-283, 'K',285-289, 'R',29 C.Genetics: A.Genetics: A.Genes obb. ATF4; TXREB; TAXREB67; CRE A.Genes references: GDB:132551 A.Map position: 22q12.3-22q13.1 C.Keywords; DNA binding; transcription	Query Match Best Local Matches Oy 1

RESULT 2 S26812 transcription factor ATF-4 - mouse N;Alternate names: activating transcription factor 4; TAXREB67 homolog; transcription fa

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A; Status: preliminary; nucleic acid sequence not shown; translation not shown
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87.5%;
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Best Local Similarity 87.55,
7; Conservative
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Best Local Similarity
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A;Molecule type: DNA
A;Residues: 1-350 <ARN>
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Proc. Natl. Acad. Sci. U.S.A. 89, 5789-5793, 1992
Proc. Natl. Acad. Sci. U.S.A. 89, 5789-5793, 1992
Aritle: Protein interaction cloning in yeast: identification of mammalian proteins that A.Refession communer: A46132; MUID:92335183; PMID:1631061
A.Refession: C46132
A.Refession: C46132
A.Refession: C46132
A.Residues: acid sequence not shown; not compared with conceptual translation A.Residues: 246-381 cHE1>
A.Residues: 246-381 cHE1>
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A.Residues: C46-381 cHE1>
A.Residues: C46-381 cHE1>
A.Residues: C46-381 cHE1>
A.Ross-references: GB:M94087; NID:g293723
A.Ross-reference extracted from NCBI backbone (NCBIP:108537)
Submitted to GenBank, November 1994
                                                                                                                                                                                                                                                               A;Cross-references: EMBL:X61507; NID:g50049; PIDN:CAA43723.1; PID:g50050
R;Mielnicki, L.M.; Pruitt, S.C.
Nucleic Acids Res. 19, 6332, 1991
A;Title: Isolation and nucleotide sequence of a murine cDNA homologous to human activati
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A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 'MSFLNSEVLAGOLMS',51-381 < CHE2>
A; Cross-references: GB:M94087; NID:g293723; PIDN:AAA53043.1; PID:g567226
A; Experimental source: strain CD-1, embryo
A; Note: the submission of the complete sequence to GenBank is mentioned in reference A46
R; Valleio, M.; Ron, D.; Miller, C.P.; Habener, J.F.
Proc. Natl. Acad. Sci. US.A. 90, 4679-4683, 1993
A; Title: C/AFF, a member of the activating transcription factor family of DNA-binding pr
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C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: H64657
|Species: Mus musculus (house mouse)
|Jate: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
|Accession: S26812; S18719; C46132; A58861; A47443
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Kresidues: 'MTBNSTLNSEVLAGDLMS',51-376,'Q',378-381 <VAL>
A;Cross-references: GB:L13791, NID:g293841; PIDN:AAA40476.1; PID:g293842
C;Keywords: transcription factor
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Fred. No. 0.22;
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                                                                                            R,Pruitt, S.C.
submitted to the EMBL Data Library, August 1991
A,Reference number: S26812
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-57,59-288,'R',290-381 <MIE>
A;Cross-references: EMBL:X61507
R;Chevray, P.M.; Nathans, D.
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88.9%;
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Best Local Similarity
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A,Molecule type: DNA
A,Residues: 1-381 <PRU>
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Zinc-dependent alcohol dehydrogenase - Helicobacter pylori (strain J99)
C.Species: Helicobacter pylori
A;Variety: strain J99 |
A;Variety: strain J99 |
B;Variety: strain J99 |
A;Molecule,type: DNA
A;Residues: 1.348 <TOM>
A;Cross-references: GB:AE000617; GB:AE000511; NID:g2314256; PIDN:AAD08150.1; PID:g231425
C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
C;Keywords: alcohol metabolism; metalloprotein; oxidoreductase; zinc
C;Keywords: alcohol metabolism; dehydrogenase homology <LADH>
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A;Experimental source: strain J99
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A,Experimental source: strain VF5
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A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: D70485
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Residues: 1-191 <AQF>
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C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 18-Jun-1999
C;Accession: D70485
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C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase
F;27-335/Domain: long-chain alcohol dehydrogenase homology <LAD>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 78.2%; Score 43; DB 1; Length 348; Local Similarity 87.5%; Pred. No. 2.5; nes 7; Conservative 0; Mismatches 1; Indels
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Pred. No. 2.5;
0; Mismatches 1; Indels
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5-phosphoribosyl-4-(N-succinocarboxamide)-5-aminoimidazole synthetase - moth bean C;Species: Vigna aconitifolia (moth bean)
C;Species: Vigna aconitifolia (moth bean)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 03-Mar-1995
C;Accession: 845524
R;Chapman, K.A.; Delauney, A.J.; Verma, D.P.S.
R;Chapman, K.A.; Delauney, A.J.; Verma, D.P.S.
A;Description: De novo purine biosynthesis in legume root nodules: cloning and sequenci: A;Reference number: 845524
A;Accession: 845524
A;Accession: Bx1524
A;Accession: Bx1524
A;Accession: Jx1524
A;Accession: Jx1524
A;Accession: Jx1524
A;Residues: 1-341 cCHA>
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
C;Accession: G88839
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
M;Title: Genome sequence of the nematode C. elegans: a platform for investigating biologing A;Reference number: A75000; MUID:990659613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_elegans/ and www_sanger.ac.uk/Projects/ and www_sanger.ac.uk/Projects/C_elegans/ and www_sanger.ac.uk/Projects/C_elegans/ and www_sanger.ac.uk/Projects/ and www_sanger.
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                                                                                                                                                                                                                                                                                                                           A;Map position: 4
A;Introns: 40/2; 70/2; 101/3; 132/3; 176/1; 263/3; 310/2; 379/3; 427/1; 522/3; 587/3
C;Superfamily: fruit fly white protein; ATP-binding cassette homology
                          A, Accession: T19189
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-633 < WIL>
A; Residues: 1-633 < WIL>
A; Residues: 1-633 < WIL>
C; CESP: C10C6.5
A; Experimental source: clone C10C6
C; Genetics:
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100.0%; Pred. No. 20;
tive 0; Mismatches (
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Best Local Similarity 66....
Fram 6; Conservative
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Best Local Similarity 66...
6; Conservative
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457 KHFRIHGFA 465
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463 KHFRIHGFA 471
A; Reference number: 219086
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A;Molecule type: DNA
A;Residues: 1-639 <STO>
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A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Rossides: 1-2391 (FLO)
A;Cross-references: BMBL:L32150; NID:9476023; PID:9476024; PIDN:AAA29522.1
C;Superfamily: rudimentary enzyme; aspartate/ornithine carbamoyltransferase homology; Ba
C;Superfamily: rudimentary enzyme; aspartate/ornithine carbamoyltransferase homology; Ba
C;Keywords: ligase
C;Keywords: ligase
F;96-2367/Domain: carbamoyl-phosphate synthase (ammonia) homology <CPA>
                                                                                                                                                                                                                                                                                                                carbamoyl-phosphate synthase (glutamine-hydrolyzing) (EC 6.3.5.5) II - malaria parasite C;Species: Plasmodium falciparum
C;Species: Plasmodium falciparum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000
C;Accession: T18410
R;Flores, M.V.C.; O'Sullivan, W.J.; Stewart, T.S.
Submitted to the EMBL Data Library, March 1997
A;Description: Characterisation of the carbamoyl phosphate synthetase gene from Plasmodi
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C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C;Accession: AD0095
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Jil, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
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hypothetical protein C10C6.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000
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Pred. No. 15;
1; Mismatches 1; Indels
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Mismatches
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Best Local Similarity 77.8-
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HFSPYGFS 180
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Matches 6; Conserv
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A;Molecule type: DNA
A;Residues: 1-375 <KUR>
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A;Gene: YPO0774
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Matches
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21 FKPHGF 26

FKPHGF 8

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hypotherical protein F5F19.9 [imported] - Arabidopsis thaliana C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Accession: A96560
R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
A,Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Lin, X.; Liu, Z.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Attle: Sequence and analysis of chromosome I of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
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C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-411 <WIL>
A;Cross-references: EMBL:Z81015; PIDN:CAB02660.1; GSPDB:GN00028; CESP:C11E4.3
A;Experimental source: clone C11E4
                        Cispecies: Caenorhabditis elegans
Cispecies: Caenorhabditis elegans
Cipate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
Cipacession: T19195
Simbartimore, B.
Submitted to the EMBL Data Library, October 1996
A;Reference number: Z19087
A;Accession: T19195
A;Accession: T19195
A;Accession: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 411;
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hypothetical protein C11E4.3 - Caenorhabditis elegans
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Pred. No. 37;
0; Mismatches
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A;Gene: CESP:C11E4.3
A;Map position: X
A;Introns: 12/3; 91/3; 136/2; 182/3; 230/3; 307/3
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Best Local Similarity 75.vv.
6; Conservative
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tes 6; Conservative
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A; Accession: A2633
A; Accession: A2633; MUID:87291864; PMID:3616485
A; Accession: A2853; MUID:87291864; PMID:3616485
A; Accession: A285418864; PMID:36164864; PMID:36164864; PMID:36164864; PMID:36164864; PMID:36164864; PMID:36164864*
A; Accession: A28541864; PMID:36164864; PMID:36164864*
A; Accession: A28541864*
A; Accession: A28
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A,Cross-references: EMBL:U58756, PIDN:AAC48087.1; GSPDB:GN00022; CESP:F58F9.1
A,Experimental source: strain Bristol N2; clone F58F9
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C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T28848
                                                                                                                                                                                                                                  Serum amyloid A protein - horse
NiContains: amyloid protein AA
Cispecies: Equus caballus (domestic horse)
Cispecies: Equus caballus (domestic horse)
Cipate: 19-Nov-1988 #sequence_revision 12-Feb-1993 #text_change 17-Mar-1999
CiAccession: A60430; A28573
Risletten, K.; Husebekk, A.; Husby, G.
Scand. J. Immunol. 30, 117-122, 1989
A; Title: The primary structure of equine serum amyloid a (SAA) protein.
A; Reference number: A60430; MUID:89332320; PMID:2502829
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1; Mismatches

Query Match 67.3° Best Local Similarity 83.3° Matches 5; Conservative

100 HFRPHG 105

2 HFKPHG 7

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Conservative

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2 HFKPHGFS

Query Match Best Local Similarity 6; Conserv

A; Map position: 4

179 NFKPHGIS 186

R;Nelson, J.; Wohldmann, P. submitted to the BMBL Data Library, May 1996 submitted to the BMBL Data Library, May 1996 A;Description: The sequence of C. elegans cosmid F58F9. A;Reference number: Z20531

A, Accession: T28848 A, Status: preliminary; translated from GB/EMBL/DDBJ A, Molecule type: DNA

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A:Accession: T29884
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Mossiques: 1-668 (ANHA>
A;Cross-references: EMBL:U51997; PIDN:AAC48156.1; GSPDB:GN00028; CESP:F19G12.2
A;Experimental source: strain Bristol N2; clone F19G12
A;Genetics:
A;Gene: CESP:F19G12.2
A;Map position: X
A;Introns: 444/3; 561/2
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Search completed: December 16, 2003, 14:19:19 Job time : 11.3333 secs

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KHFKPHGFS
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Q86f69 mus musculu
Q61328 mus musculu
Q25732 helicobacte
Q9zka9 helicobacte
Q9712 aquifex aeo
Q9DyM3 plasmodium
Q21732 plasmodium
Q27732 plasmodium
Q87732 plasmodium
Q87732 plasmodium
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08vzw9 vigna ungui
09vpw4 drosophila
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                                             December 16, 2003, 14:09:45; Search time 25 Seconds (without alignments) 92.899 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                          830525 seqs, 258052604 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                 OM protein - protein search, using sw model
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Q8CF69
Q8CF69
Q8CF32
Q9CKA9
Q9CKA9
Q9CF83
Q8CHV3
Q8CHV7
Q9CSFP3
Q9CNF9
Q9CP94
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p_vertebrate:*
o_unclassified:*
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sp bacteria:*
sp bucteria:*
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sp human:*
sp nvertebrate:*
sp mammal:*
sp organelle:*
sp phage:*
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seq length: 200000000
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sp_rodent:*
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Match Length
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Perfect score:
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99noy equus cabal
088595 xanthomonas
990790 mus musculu
090180 pasteurella
02093 caenorhabdi
091305 caenorhabdi
023831 arabidopsis
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Q9ssv0 arabidopsis
Q9ssv0 arabidopsis
Q9mwy arabidopsis
Q97ui4 sulfolobus
Q8eens shewanella
Q8eens shewanella
Q8xsv ralstonia s
Q9xq8 drosophila
Q9vq8 drosophila
Q6vq8 drosophila
Q9vq8 drosophila
Q9mg8 rhizobium l
Q9mg8 rhizobium l
P72417 salmonella
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Q9lif1 lymantria d
Q9lim2 arabidopsis
Q933e7 helicobacte
Q98tp6 platichthys
Q9K9N9 bacillus ha
O34743 bacillus su
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09gsz6 plasmodium 09gsz7 plasmodium
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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Nehring R.B:, Horikawa H.P.M., El Far O., Kneussel M.,
Brandstatter J.H., Stamm S., Wischmeyer E., Betz H., Karschin A.;
"The Metabotropic GARAB Receptor Directly Interacts with the
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PROSITE; PS0036; BZIE BASIC; 1.
DNA-binding; Nuclear protein.
SRQUENCE 347 AA; 38151 MW; CCE6BD02F263296B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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J. Biol. Chem. 275:35185-35191 (2000).
-!- SIMILARITY: BELONGS TO THE BZIP FAMILY.
EMBL, AF555627; AAG31732.1;
InterPro; IPR004827; TF bZIP.
Pfam; PF00170; bIIP; 1.
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                             Q9N0Y1
Q8P5G5
Q9D7Q0
Q9CL80
Q20993
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Q9N8B2
Q9VC4B
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Q9K9N9
Q34743
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Q9SSV0
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Q8E8N8
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Q98MP8
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10116;
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Q96AQ3

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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Activating TRANSCRIPTION factor 4 (Activating TRANSCRIPTIONN factor 4)
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STRAIN=26695 / ATCC 700392;

STRAIN=2739467; PubMed=9252185;

Tomb J.-F., White O., Kerlange A.R., Clayton R.A., Sutton G.G.,

Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,

Nelson K., Quackenbush J., Zhou L., Kirkness B.F., Peterson S.,

Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,

McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,

Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,

Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.,
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H21104.
H21icobacter pylori (Campylobacter pylori).
H21icobacteraceae; H21icobacter.
NCBI_TaxID=210;
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MEDLINE=92183900; PubMed=1371974;
Mishizawa M., Nagata S.;
"cDNA clones encoding leucine-zipper proteins which interact with CSF gene promoter element 1-binding protein.";
FEBS Lett. 299:36-38(1992).
                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=129/SV;
MEDLINE=22066493; PubMed=1956797;
Michlicki L.M., Pruitt S.C.;
"Isolation and nucleotide sequence of a murine cDNA homologous to human activating transcription factor 4.";
                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 49; DB 11; Length 381;
Pred. No. 0.5;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nishizawa M., Nagata S.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF001/0; DELL; 1.
SNART; SM0038; BRIZ; 1.
PROSITE; PS00036; BZIP_BASIC; 1.
DNA-binding; Nuclear protein.
THE STATE ABI AB; 91810 MW; 9FC3A0CA16EB7431 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
clinamyl-alcohol dehydrogenase ELI3-2 (CAD).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  348 AA.
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EMBL; X61507; CAA43723.1; -.
EMBL; AB012277; BAA25314.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic Acids Res. 19:6332-6332(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 119-381 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSFAC; T02052; -.
MGD; MGI:88096; Atf4.
InterPro; IPR004827; TF bZIP.
Pfam; PF00170; bZIP: 1.
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Best Local Similarity 88.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 KHLKPHGFS 82
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                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                            ATF4 OR ATF-4.
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MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium.
The FANTOM Consortium.
The FANTOM Consortium.
The RANTOM Consortium Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
EMBL; AKO03001; BAC25014.1; -.
SEQUENCE 350 AA; 38715 MW; 6394500297E6C3CE CRC64;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                      Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUE=vvary, and Colon;
Strausberg R.,
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE BZIP FAMILY.
BMDL; BCO1688; AAH16555.1; -.
EMBL; BCO1688; AAH22088.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00338; BRLZ; 1.
PROSTRE; PS00036; BZIP BASIC; 1.
Hypothetical protein; DNA-binding; Nuclear protein.
SEQUENCE 351 AA; 38589 MW; 3BBB7379DC3B0D07 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Activating transcription factor 4.
                                                                                                                                  Last sequence update)
Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Created)
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Pfam; PF00170; bZIP; 1.
                                                                                                    01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2003 (TrEMBLrel. 23,
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                                                PRELIMINARY;
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                                                                                                                                                                                        Hypothetical protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KHFKPHGFS 50
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Best Local Similarity
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RESULT 3

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RESULT 4 Q61328 ID Q6133 AC Q6133 DT 01-N

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Query Match

Matches

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Gaps

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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Carbamoyl phosphate synthetase II (EC 1.4.3.6) (Copper amine oxidase)
(Fragment).
                                                                                                                                                                                                                                                         Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Shead M.A., Keller M., Aujay M., Huber R., Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; "The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Katrib M.T., Stewart T.S.;
"Carbamoyl phosphate synthetase II gene from Plasmodium vivax.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: RCH(2)NH(2) + H(2)0 + O(2) = RCH0 + NH(3)
-!- COFACTOR: BINDS 1 COPPER ION AND 1 TOPAQUINONE PER SUBUNIT (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY).
-!- SIMILARITY: BELONGS TO THE COPPER/TOPAQUINONE OXIDASE FAMILY.
EMBL; AF327646; AAK15525.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmodium vivax.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
NCBI_TaxID=5855;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74.5%; Score 41; DB 16; Length 191; 66.7%; Pred. No. 7.6; ive 2; Mismatches 1; Indels
                                                                                                                                 Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
NCBL_TaxID=63363;
                                                                                                                                                                                                                                                                                                                                                                                                               Premi, PP012307, HIT; 1.
Hypothetical protein; Complete proteome.
REQUENCE 191 AA; 22403 MW; EFA14A8699BB9165 CRC64;
          01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
11-ANR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein AQ_2159.
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PROSITE; PS01164; COPPER AMINE_OXID_1; 1.
PROSITE; PS00867; CPSASE_2; 1.
PROSITE; PS00430; TONE_DEPENDENT_REC_1; 1.
Copper; Oxidoreductase; TPQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HASSP, PO0568; 1A9X.
InterPro; IPR005483; CPase_L.
InterPro; IPR005480; CPase_L_D2.
InterPro; IPR005480; CPase_L_D3.
InterPro; IPR00559; CuMH oxidase.
InterPro; IPR000531; TonB boxC.
Pfam; PF02786; CPasee_L_D2; 1.
Pfam; PF02787; CPasee_L_D2; 1.
                                                                                                                                                                                                                         STRAIN=VF5;
MEDLINE=98196666; PubMed=9537320;
                                                                                                                                                                                                                                                                                                                                                       Nature 392:353-358(1998).
EMBL; AE000776; AAC07886.1; -.
InterPro; IPR001310; HIT.
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Best Local Similarity 66...
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119 KEYKPHGFN 127
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                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                     Aquifex aeolicus
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                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                         Nature 388:539-547(1997).
-!- COFACTOR: REQUIRES ZINC FOR ITS ACTIVITY (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99120557; PubMed=9923682; Alm R.A., Ling L.S.L., Brown B.D., Doig P.C., Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown B.D., Doig P.C., Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G. Turmino P.J., Caruso A. Uria-Nickelsen M., Mills D.M., Ives C., Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gastric pathogen Helicobacter pylori.";
Nature 397.17-180(1939).
-i- COFACTOR: REQUIRES ZINC FOR ITS ACTIVITY (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genomic sequence comparison of two unrelated isolates of the human
                                       "The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
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                                                                                                                                                      EMBL, AEGOGIT, AADO8150.1; -.
TIGR; HP1104; -.
InterPro; IPRO22328; ADH_zinc.
InterPro; IPRO2085; Adh_zn_family.
PROSITE; PSO0059; ADH_ZINC; 1.
Hypothetical protein; Oxidoreductase; Zinc; Complete proteome.
SEQUENCE 348 AA; 38645 MW; 07D7E1A63048EF48 CRC64;
Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                  78 2%; Score 43; DB 16; Length 348; 87.5%; Pred. No. 5.9; artive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78.2%; Score 43; DB 16; Length 350; 87.5%; Pred. No. 5.9;
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InterPro; IRR0020328; ADH zinc.
InterPro; IRR002085; Adh zn_family.
Pfam; PF00107; adh_zinc; -1.
PROSITE; PS00059; ADH_ZINC; 1.
Oxidoreductass, zinc; Complete proteome.
SEQUENCE 350 AA; 38939 MW; OCC26211002E6CD1 CRC64;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-2002 (TrEMBLrel. 20, Last annotation update)
Zinc-dependent alcohol dehydrogenase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  350 AA
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nes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 HPKPHDFS 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 HFKPHGFS 9
                                                                                                                                                                                                                                                                                                                                                                                                                          2 HFKPHGFS 9
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                         Venter J.C.;
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                                                                                                                                          FAMILY
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SEQUENCE 1
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Harris B., Lennard N., Clark L., Line A., Barron A., Corton C.,
Berriman M., Pain A., Hall N., Arkin R., Chillingworth C., Doggett J.,
Ormond D., Sanders M., Hayes R., Hall S., Quail M., Barrell B.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AL844509; CAD52216.1; -.
                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H(2)O(2).
-!- COFACTOR: BINDS 1 COPPER ION AND 1 TOPAQUINONE PER SUBUNIT (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=FCQ27;
Plores M.V.C., O'Sullivan W.J., Stewart T.S.;
"Characterisation of the Carbamoyl Phosphate Synthetase Gene from Plasmodium falciparum.";
Submitted (MAX-1994) to the EMBL/GenBank/DDBJ databases.
-:- CATALYTIC ACTIVITY: RCH(2)NH(2) + H(2)O + O(2) = RCHO + NH(3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: BELONGS TO THE COPPER/TOPAQUINONE OXIDASE FAMILY.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Carbamoyl phosphate synthetase II (BC 6.3.5.5) (Copper amine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 41; DB 5; Length 2375; Pred. No. 94;
                                                                                  Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2375 AA; 273435 MW; 398D3D5E9DBA24D1 CRC64;
    321 AA; 36844 MW; 6C5001566CDC5E8A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
101-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Carbamoyl phosphate synthetase, putative (EC 6.3.5.5)
                                                                                  2.
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                                                                                  74.5%; Score 41; DB 77.8%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                            1; Mismatches
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Plasmodium falciparum (isolate 3D7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74.5%;
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Best Local Similarity 77...
7; Conservative
                                                                                                                                                                    Conservative
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1154 KYFKKHGFS 1162
                                                                                                                                                                                                                                                                                                                        267 KYFKKHGFS 275
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les 7; Conserv
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SEQUENCE
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            SEQUENCE
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                                                                                          Query Match
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Q27732;
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Q8IEN3;
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STRAIN=KIM5 / Biovar Mediaevalis;
MEDILINE=21137865; PubMed=12142430;
Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
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MEDLINB=21470413; PubMed=11586360;
Parkhill J., Waren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,
Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
"Genome sequence of Yersinia pestis, the causative agent of plague.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Enterobacteriaceae; Yersinia.
NCBI_TaxID=632;
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PRINTS; PR00099; CPSGATASE.

PRINTS; PR00099; CPSGATASE.

PRINTS; PR00099; CPSGATASE.

TIGRFAMS; TIGR01369; CPSGASEIIsmall; 1.

PROSITE; PS01164; COPPER_AMINE_OXID_1; 1.

PROSITE; PS00867; CPSASE 1; 1.

PROSITE; PS00016; EF AMINE_OXID_1; 1.

PROSITE; PS00018; EF AMINE_OXID_1; 1.

PROSITE; PS00018; EF AMINE_OXID_1; 1.

PROSITE; PS00018; EF AMINE_OXIGOTED_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2002 (TYENBLYEL 20, Last sequence update)
1-MAR-2003 (TYENBLYEL 23, Last annotation update)
1-MAR-2003 (TYENBLYEL 23, Last annotation update)
1-MAR-2003 (TYENBLYEL)
1-MAR-2003 (TYENBLYEL)
1-MAR-2007 (TYENBLYEL)
1-MAR-2007 (TYENBLYEL)
1-MAR-2007 (TYENBLYEL)
1-MAR-2002 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         375 AA
                                                                                                        InterPro; IPR005483; CTase_L.
InterPro; IPR005479; CPase_L.D2.
InterPro; IPR005480; CPase_L.D2.
InterPro; IPR005481; CPase_L.N.
InterPro; IPR005491; CPase_E.M.
InterPro; IPR001317; CPS_GATase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00289; CPSase L. Chain; 2. Pfam; PF02786; CPSase L. D2; 2. Pfam; PF02787; CPSase L. D3; 1. Pfam; PF00989; CPSase Sm_chain; 1. Pfam; PF00117; GATase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interpro; IPR000269; CuNH_oxidase.
Interpro; IPR002048; EF-hand.
Interpro; IPR000991; GATasa.
Interpro; IPR004362; MGS_like.
InterPro; IPR006275; CarA_L_glu.
InterPro; IPR006274; CarA_small.
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Best Local Similarity 77.00.,
And 77 Conservative
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Gaps

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Martinez-Arias R., Henne A., Wiezer A., Baeumer S., Jacobi C., Brueggemann H., Lienard T., Christmann A., Boemecke M., Steckel S., Bhattacharya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus R.P., Fritz H.-J., Gottschalk G., "The genome of Methanosarcina mazei: evidence for lateral gene transfer between Bacreria and Archaea "; J. Mol. Microbiol. Biotechnol. 4:453-461(2002). BRBL, AB012251, AAM29846.1; -Complete protecome: Hypotherical protein. SEQUENCE 289 AA; 32222 MW, AF59E9997E30ADF6 CRC64;
                                                                                                                                                                                                                                                                  Score 38; DB 17; Length 289;
Pred. No. 41;
                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              il protein; Complete proteome 317 AA; 33877 MW; 7705D7161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=1021;
MEDLINE=21396507; PubMed=11481430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 98
EMBL; ALS1789; CAC46529.1; -
InterPro; IPROQU3304; FMCA, AmdA.
Pfam; PF03069; FMCA, AmdA, AmdA.
Hypothetical protein; Complete p
                                                                                                                                                                                                                                                                         69.1%;
66.7%;
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Best Local Similarity 66.7%,
6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                     249 KHYDEHĞFS 257
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Brubaker C.L., Liu Q., Green A.G., Marshall D.R., Singh S.P.;

Brubaker C.L., Liu Q., Green A.G., Marshall D.R., Singh S.P.;

"Microsomal omegaé desaturase intron topologies contribute to our
understanding of reticulate evolution in Gossypium (Malvaceae) and the
evolution of the Australian Gossypium species.";

Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ244917, CABS9280.1; -.
NON TER 1
     Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V., Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gossypium stocksii.
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                              6
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                                                                                                                                                                                                                                           Score 39; DB 16; Length 375;
Pred. No. 35;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 38; DB 10; Length 51;
Pred. No. 7.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MICROSOMAL OMEGA6 DESATURASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
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                                                                    "Genome sequence of Yersinia pestis KIM.";
J. Bacteriol. 184:4601-4611(2002).

EMBL; AJ41444; CAC89623.1; --
EMBL; ABC103944; AAM86968.1; --
Hypothetical protein; Complete proteome.

SEQUENCE 375 AA; 41623 MW; AAIF781311AC9ABO CRC64;
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STRAIN=Goel / Gol / ATCC BAA-199 / DSM 3647 / OCM 88;
MEDLINE=22120827; PubMed=12125824;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B3103EFF7594E8A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
Microsomal omega6 desaturase enzyme (Fragment).
PAD2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                              70.9%;
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5728 MW;
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                                                                                                                                                                                                                                           Query Match
Best Local Similarity 75.0
Matches 6; Conservative
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KPFRPHGF 46
                                                                                                                                                                                                                                                                                                                                              2 HFKPHGFS 9
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                                                Perry R.D.;
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1D QSSME3

1D QSSME3

DT 01-MAY-

DT 01-MAY-

DT 01-MAY-

DE Microsol

GN Gossypi.

CC Spermath

CC S
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J., Boistard P., Becker A., Boutry M., Cadieu B., Dreano S., Gloux S., Goiteur T., Goffeau A., Rahn D., Kiss E., Lelaure V., Masuy D., Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U., Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F., "Analysis of the chromosome sequence of the legume symbiont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
0
                                                                                                                                                                                    R01950 OR SMC04290.
Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2002 (TrEWBLrel. 20, Created)
01-MAR-2002 (TrEWBLrel. 20, Last sequence update)
01-OCT-2002 (TrEWBLrel. 22, Last annotation update)
Succinoaminoimidazolecarboximide ribonucleotide synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7705D716F6B9EE2A CRC64;
                                                                                   01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) Hypothetical protein R01950.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sinorhizobium meliloti strain 1021.";
Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69.1%; Score 38; DB 16; 75.0%; Pred. No. 45; ive 1; Mismatches 1
317 AA.
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OC curceids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.

RN 11

RP 131

RP 131

RP 25DUENCE FROM N.A.

RC STAINECY. Vita 3;

RA Smith P.M.C., Mann A.J., Reck V.;

RT "Vupur7 mRN4 from cowpea encoding succinoaminoimidazolecarboximide

RT Tibonucleotide synthetase.";

RI Submitted (NOV-2001) to the FEMEL/GenBank/DDBJ databases.

CC -!- CATALYIIC ACTIVITY: ATP + 5-AMINO-1-(5-FHOSPHO-D-

RIBOSYLIMINDAZOLE-4-CARBOXVIATE + L-ASPARTATE = ADP + PHOSPHATE +

(S)-2-[5-AMINO-1-(5-FHOSPHO-D-RIBOSYL) IMIDAZOLE-4-

CC -!- PATHWAY: DE NOVO PURINE BIOSYNTHESIS; SEVENTH STEP.

CC -!- PATHWAY: DE NOVO PURINE BIOSYNTHESIS; SEVENTH STEP.

CC -!- STAILARITY: BELONGS TO THE SAICAR SYNTHETASE FAMILY.

DR FROILSS; SAICAR SYNT: 1.

DR PROSITE; PRO1057; SAICAR SYNT: 1.

DR ROSITE; PRO1057; SAICAR SYNTHETASE 1; 1.

DR ROSITE; PRO1057; SAICAR SYNT: 1.

RW Ligase; Purine biosynthesis.

QUery Match

Best Local Similarity 100.0%; Pred. No. 57;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 FKRHGF 8
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Search completed: December 16, 2003, 14:18:04 Job time: 26 secs

38 FKPHGF 43

qq

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S. epidermidis opermuman angiopoietin Human angiopoietin Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Human polypeptide M. tuberculosis an Mycobacterium tube M. tuberculosis an Mycobacterium tube M. tuberculosis an Mycobacterium tube T. gondii immunoge Mouse ageing inhib Streptococcus pneu Etreptococcus pneu Human protein ageulus Novel human diagno Herbicidally activ Streptococcus pneu Streptococcus spneu Streptococcus spneu Streptococcus spneu
                                Drosophila melanog
Drosophila melanog
Listeria monocytog
Drosophila melanog
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S. pneumoniae type
Prophenol oxidase.
Staphylococcus epi
Mouse ageing inhib
Human novel foetal
          colon cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; cancer antigen; ATF4; CREB-2; vaccine; cytostatic; immunogenic ligand; gene therapy; MHC; major histocompatibility complex; adoptive immunotherapy; cancer; ovarian cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human cancer antigen ATF4/CREB-2 based immunogenic ligand #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
                                ABB66825
ABB69124
                                                                                                                   AAG42515
AAG44592
AAG61759
AAO02856
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ABG06198
ABB91307
                                                                                                                                                                                           AAU08121
ABG77968
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ABU02579
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AAU21269
                                                                                            AAM00213
AAB64578
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AAY29981
                                                                     ABB57998
                                                                                                                                                                                                                     AAY29080
                                                                                                                                                                                                                                                                                                                                                                                                    AAB73665
                                                          ABB49129
                                                                                                                                                                    AAW73761
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 30-MAY-2001; 2001WO-US17454.
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20-DEC-2000; 2000US-257007P
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WO200192306-A2.
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Synthetic.
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 Human cancer antig
Drosophila melanog
Bombyx mori (pro)p
Human G protein-co
G protein-coupled
Herbicidally activ
Human cancer antig
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                                                                              December 16, 2003, 14:06:05; Search time 33 Seconds (without alignments) 43.289 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                            A Geneseq 19Jun03:*

| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA41981.DAT:*
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                                                                                                                                                                                                                                        1107863
          GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                        Potal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                 1107863 segs, 158726573 residues
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Maximum Match 100%
Listing first 45 summaries
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AAU25704
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AAU74683
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AAU74684
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Gapop 10.0 , Gapext 0.5
                                                        protein search, using
                                                                                                                                                                                                                                                               seq length: 0
seq length: 2000000000
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232272323
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Match Length
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693
184
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Maximum DB
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Perfect
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contracted in vitro or in vivo in the presence and at the expense of an antigen presenting cell that presents the immunogenic compound in the contract of an MHC (major histocompatibility complex) molecule and a method of adoptive immunotherapy comprising administering the immune effector cell. The compounds are useful for modulating an immune response to the synthetic and naturally occurring compounds. The compounds are especially useful in gene therapy or as components of anti-cancer vaccines. The compounds are also useful for generating antibodies that specifically recognise and bind to these molecules. These artibodies are further useful for immunotherapy when administered to a subject. The peptides, polypeptides and polynucleotides are useful in immunotherapy when administered to a subject: methods, for the detection and purification of antibodies, or as immunogens for the production of antibodies. The present
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                                                                                                                The invention relates to compounds comprising an immunogenic ligand whose sequence is based in part on residues 42-50 of human cancer antigen ATF4/CREB-2 (not defined) and the polynucleotides encoding them. Also included are an antibody that specifically recognises and binds the compound, a method for inducing an immune responses in a subject by delivering the compound, a method of immunotherapy comprising administering to a subject the antibody, an immune effector cell that has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 respectively
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
      useful for
New therapeutic compounds comprising immunogenic ligands, useful modulating an immune response, particularly for treating ovarian cancer, and as components of anticancer vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           degeneracy of the DNA sequences.
                                                                                Claim 1; Page 55; 68pp; English
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11-JUL-2000; 2000US-0614150.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                       The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ABBS7737-ABB72072).
The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from WIPO
                                                                                        New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
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                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 12174; 21pp + Sequence Listing; English.
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Pred. No. 39;
2; Mismatches 0; Indels
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Similarity 71.4%;
5; Conservative
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20-DEC-2000; 2000US-257007P.
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WPI; 2001-656860/75.
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Best Local Similarity
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                            N-PSDB; ABL05897
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Synthetic.
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Gaps

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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The B. mori silkworm larvae derived (pro)phenoloxidases Phe52-Val693 (AAR89114) and Phe52-Gly685 (AAR89115), are encoded by AAT10240 and AAT10241, respectively. The (pro)phenoloxidases can be used as new labelling oxidases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Pro)phenol:oxidase from silkworm - useful as a labelling oxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Silkworm; larvae; pro; phenoloxidase; Phe52-Val693; Phe52-Gly685
                                                                                                                                                                                                                      Length 683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 693;
                                                                                                                                                                                                       Score 40; DB 22; Length oc. Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 40; DB 17; Length 69
Pred. No. 1.3e+02;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bombyx mori (pro)phenoloxidase Phe52-Val693.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "peptide fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "peptide fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Pages 11-14; 29pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                 AAR89114 standard; Protein; 693 AA
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                                                                                                                                                                                                                       70.2%;
71.4%;
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/note=
52..61
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Best Local Similarity
Las 5; Conserve
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403 YKWHAFI 409
                                                                                                              (ABB57737-ABB72072).
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                                                                                                                                                                                                                                                                                    3 YKWHGFV 9
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                                                                                                                                                                                          683 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           labelling oxidase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-JUN-1996
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                                                                                                                                                                                          Sequence
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                                         administering to a subject the antibody, an immune effector cell that has been raised in vitro or in vivo in the presence and at the expense of an antigen presenting cell that presents the immunopenic compound in the context of an MHC (major histocompatibility complex) molecule and a method of adoptive immunotherapy comprising administering the immune effector cell. The compounds are useful for modulating an immune response to the synthetic and naturally occurring compounds. The compounds are useful for modulating an immune response especially useful in gene therapy or as components of anti-cancer vaccines. The compounds are useful for treating cancer, particularly ovacines. The compounds are also useful for generating antibodies are further useful for immunotherapy when administered to a subject. The peptides, polypeptides and polymuleschides are useful in
Also included are an antibody that specifically recognises and binds the compound, a method for inducing an immune response in a subject by delivering the compound, a method of immunotherapy comprising
                                                                                                                                                                                                                                                  diagnostic methods, for the detection and purification of antibodies, or as immunogens for the production of antibodies. The present sequence represents a human cancer antigen ATF4/CREB-2 based immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                  respectively
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                              Note: Immunogenic ligands AAU74681-AAU74686 are stated to be encoded by the degenerate DNA sequences AAS20120-AAS20125 respect but have not been cross-referenced or CDS features put in due to degeneracy of the DNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                                                                                                                                            Score 41; DB 23; Length 5, Pred. No. 9.3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster polypeptide SEQ ID NO 5304.
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                                                                                                                                                                                                                                                                                                                                                                                                                             71.9%;
66.7%;
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                   igand of the invention.
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es 6; Conserv
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Gaps

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Phe52-Val693

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G protein-coupled receptors termed nGPCR-x. nGPCR-x polynucleotides, polypeptides, and modulators may be used in the treatment of diseases and conditions such as infections, such as vival infections caused by HIV-1 (human immunodeficiency virus) or HIV-2, pain, cancers, metabolic and cardiovascular diseases and disorders (e.g., type 2 diabetes, obesity, annotexia, hypotension, hypertension, myocardial infarction, atherosclerosis), Parkinson's disease, and psychotic and neurological disorders, including schizophrenia, migraine, major depression, anxiety, mental disorder, mannic depression, and dyskinesias, such as Huntington's disease or Tourette's Syndrome and many other diseases and syndromes listed in the specification. nGPCR-x polynucleotides and polypeptides, as well as nGPCR-x modulators, may also be used in diagnostic assays for such diseases or conditions. The present sequence represents a G protein-coupled receptor
                                                                                                                                                                                      Human; G protein-coupled receptor; nGPCR-x; antiviral; analgesic; cytostatic; cardiant; antidiabetic; anoretic; hypotensive; hypertensive; antiparkinsonian; noctropic; neuroprotective; antidepressant; viral infection; HIV-1; human immunodeficiency virus; HIV-2; pain; cancer; metabolic disease; cardiovascular disease; type 2 diabetes; obesity; anorexia; hypotension; hypertension; mycardial infarction; atherosclerosis; Parkinson's disease; psychosis; neurological disorder; schizophrenia; migraine; major depression; anxiety; mental disorder; manic depression; dyskinesia; Huntington's disease; Tourette's Syndrome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated nucleic acid molecules encoding G protein-coupled receptors termed nGPCR-x, useful in the treatment and diagnosis of viral infections, cancers and mental disorders (e.g. Parkinson's disease and
                                                                                                                                                   Human G protein-coupled receptor nGPCR-2289.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 31; Page 256; 292pp; English.
                                  AAU19356 standard; Protein; 184 AA.
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2000US-0187584.
2000US-0187637.
2000US-0187639.
2000US-0187640.
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08-MAR-2000; 2000US-0187708.
08-MAR-2000; 2000US-0187709.
08-MAR-2000; 2000US-0187827.
08-MAR-2000; 2000US-0188290.
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                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                              04-DEC-2001
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                                                                         AAU19356;
RESULT 6
                    AAU19356
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the invention

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                                                                                                                                                                                                                                                                                                                                                                Human; mental disorder; thyroid disease; renal failure; anorexia; inflammatory condition; Crohn's disease; rheumatoid arthritis; HIV; autoimmune disorder; schizophrenia; migraine; stroke; dementia; obesity; depression; Parkinson's disease; Alzheimer's disease; viral infection; thutington's disease; human immunodeficiency virus; type 2 diabetes; anorexia; hypotension; hypetrenion; thrombosis; myocardial infarction; atherosclerosis; cancer; sexual dysfunction; G protein-coupled receptor;
                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for use in the treatment of mental disorders, such as Alzheimer's
lisease, or Parkinson's disease -
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                                           66.7%; Score 38; DB 22; Length 184; 44.4%; Pred. No. 73;
                                                                             2; Indels
                                                                             3; Mismatches
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                                                                                                                                                                                                                                                                                                                                    G protein-coupled receptor, nGPCR-2118.
                                                                                                                                                                                                                                  AAU25704 standard; Protein; 220 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-FBB-2000; 2000US-0184602.
24-FBB-2000; 2000US-0184604.
24-FBB-2000; 2000US-0184606.
24-FBB-2000; 2000US-0184689.
24-FBB-2000; 2000US-0184690.
24-FBB-2000; 2000US-01847110.
24-FBB-2000; 2000US-01847112.
24-FBB-2000; 2000US-01847112.
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                                                             44.48;
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                                                                              4; Conservative
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                                           Query Match
Best Local Similarity
                                                                                                              1 FLYKWHGFV
              184 AA;
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               Sequence
                                                                              Matches
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Human, cancer antigen; ATF4; CREB-2; vaccine; cytostatic; immunogenic ligand; gene therapy; MHC; major histocompatibility complex; adoptive immunotherapy; cancer; ovarian cancer.

30-MAY-2001; 2001WO-US17454.

WO200192306-A2.

06-DEC-2001,

sapiens

Synthetic.

31-MAY-2000; 2000US-209388P. 20-DEC-2000; 2000US-257007P.

(GENZ) GENZYME CORP.

WPI; 2002-097764/13.

Nicolette CA;

Human cancer antigen ATF4/CREB-2 based immunogenic ligand #3.

(first entry)

09-APR-2002

AAU74683;

AAU74683 standard; Peptide; 9 AA.

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 \begin{array}{c} \mathbf{x} \\ \mathbf{x} \\ \mathbf{y} \\ \mathbf{x} \\ \mathbf{y} \\ \mathbf{x} \\ \mathbf{y} \\ \mathbf{x} \\ \mathbf
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atherosclerosis, cancer, and sexual dysfunction. AAU25617-AAU25726 represent the amino acid sequences of novel human G protein-coupled receptors, nGPCR-2031 to nGPCR-2140 respectively, as described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                Score 38; DB 22; Length 220;
Pred. No. 87;
1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Herbicidal; plant; agriculture; herbicide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB92481 standard; Protein; 448 AA.
                                                                                                                                                                                                                                                                                                                                66.78;
                                                                                                                                                                                                                                                                                                                                                                             66.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-AUG-2001; 2001WO-EP09892
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                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
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84 FLNLWHGFL 92
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                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                   220 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200210210-A2
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                                                                                                                                          invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB92481;
                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                     Query Match
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New therapeutic compounds comprising immunogenic ligands, useful for modulating an immune response, particularly for treating ovarian cancer, and as components of anticancer vaccines

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The invention relates to compounds comprising an immunogenic ligand whose sequence is based in part on residues 42-50 of human cancer antigon ATF4(FRB-2 (not defined) and the polynucleotides encoding them. Also included are an antibody that specifically recognises and binds the compound, a method for inducing an immune response in a subject by delivering the compound, a method of immunotherapy comprising cadministering to a subject the antibody, an immune effector cell that has been raised in vitro or in vivo in the presence and at the expense of an entition presenting cell that presents the immunogenic compound in the context of an MHC (major histocompatibility complex) molecule and a method of adoptive immunotherapy compunies the immune response of context of an MHC (major histocompatibility complex) molecule and a method of adoptive immunotherapy compounds. The compounds are useful for modulating an immune response of the synthetic and naturally occurring compounds. The compounds are useful for treating cancer, particularly covarian cancer. The compounds are also useful for generating antibodies that specifically recognise and bind to these molecules. These compounds are also useful for generating antibodies chart specifically recognise and bind to these molecules. These cusptides are also useful for antibodies are useful in diagnostic methods, for the detection and purification of antibodies. The present correct antigen ATF4(CRBP-2 based immunogenic interview) is an antibodies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 9.3e+05;
1; Mismatches 2; Indels
Claim 3; Page 55; 68pp; English.
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Best Local Similarity 66.7
Matches 6; Conservative
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Gaps

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Score 38; DB 23; Length 448; Pred. No. 1.8e+02; 0; Mismatches 2; Indels

66.7%; 75.0%;

Query Match Best Local Similarity

448 AA;

Seguence

Conservative

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Matches

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FLYKWHGF

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FLYPWFGF 15

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RESULT

Human; colon cancer; colon cancer antigen; diagnosis; detection; colorectal carcinoma; chromosome 17.

Rosen CA;

Birse CE,

Ruben SM, Barash SC, WPI; 2001-235357/24.

N-PSDB; AAH33877

(HUMA-) HUMAN GENOME SCI INC.

99US-0157137. 99US-0163280.

29-SEP-1999;

28-SEP-2000; 2000WO-US26524

WO200122920-A2 Homo sapiens.

05-APR-2001.

Human colon cancer antigen protein SEQ ID NO:5210.

(first entry)

03-SEP-2001

AAG74446 standard; Protein; 92 AA.

1 FLHKWHWVV 9

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forensic; gene therapy; chromosome mapping; signal peptide; prostate; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; haematopoiesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition.
                                                                                Human; secreted protein; EST; expressed sequence tag; diagnosis;
                                                              Human 5' EST secreted protein SEQ ID No: 530,
                                                                                                                                                                                                                                                         Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                          Claim 34; Page 636; 675pp; English.
         AAY11930 standard; Protein; 23 AA.
                                                                                                                                                                                                     98WO-IB01232.
                                                                                                                                                                                                                       97US-0905144.
                                            18-JUN-1999 (first entry)
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Best Local Similarity
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                                                                                                                                                                                                                                                                                      N-PSDB; AAX40652
                                                                                                                                                                                                                                       (GEST ) GENSET
                                                                                                                                                                                                     31-JUL-1998;
                                                                                                                                                                WO9906550-A2
                                                                                                                                                                                                                       01-AUG-1997;
                                                                                                                                                Homo sapiens
                                                                                                                                                                                   11-FEB-1999.
                                                                                                                                                                                                                                                          Duclert A,
                           AAY11930;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. Nad P may be used in the prevention, adaquosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, inscring the nucleic acids into a host cell and culturing the cell color express the proteins. N and P can be used in the prevention, diagnosis and AAB77789 represent sequences used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diagnosing and/or treating colorectal cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present invention.

N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11; Page 6892-6893; 9803pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             useful for preventing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |:||| |
6 LFKWHNF 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                can be used in forensic, gene therapy and chromosome mapping procedures. The sequences can also be used for obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptides can be used for directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a membrane, or importing a polypeptide into a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAX40438 to AAX40715 represent 5' expressed sequence tags (ESTs) for human secreted proteins expressed in prostate, and encode the proteins given in AAV17191 to AAV11993 respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The nucleic acid sequences can be used for products for diagnosis and therapy. The proteins obtained may have cytokine activity, cell proliferation and differentiation activity, haematopoissis regulating activity, tissue growth regulating activity, nemestatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, tumour inhibition activity or other activity, anti-inflammatory activity, tumour inhibition activity or other activities. The products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated prostate-derived nucleic acids - used to develop products which may have cytokine, immune regulatory, haematopoiesis regulating, anti-inflammatory or tumour inhibition activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lacroix B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 13;
1; Mismatches
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FLIQWHGSV 19
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Match 64.9%; Score 37; DB 22; Length 92; Local Similarity 71.4%; Pred. No. 54; Local 5; Conservative 1; Mismatches 1; Indels
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RESULT 11

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09-AUG-2001
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Human; cytokine; cell proliferation; cell differentiation; growth factor; haematopoiesis regulation; tissue growth; immunomodulator; activin; himbin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; pymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; atterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiinflammatory; antiathmatic; antiathritic; haemostatic; antiatreriosclerotic; cytostatic; osteopathic; vascuropic; cardiant; virucide; antibacterial; antifungal; vulnerary; antiulcer.
Human LCP homologue, SEQ ID NO:1639,
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Homo sapiens.

WO200157188-A2

05-FEB-2001; 2001WO-US03800.

03-FEB-2000; 2000US-0496914. 27-APR-2000; 2000US-0560875.

(HYSE-) HYSEQ INC

Drmanac RT; Liu C, rang YT,

WPI; 2001-457740/49. N-PSDB; ABA08513 Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer

Claim 20; Page 161; 1963pp; English.

Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the bind the invention have homology to known proteins, thereby giving a insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may differentiation activities, including cytokine, cell proliferation or cell differentiation activities, stem cell growth activity; chamalopolesis regulatory activity; tissue growth activity; chemocallatory activity, activity; tissue growth activity; chemocallatory activities, receptor or inhibin-related activities; chemocallatory activities, neceptor or ligand activities, or may be involved in oncogenesis, cancer cell proliferation or metastasis. Depending on their biological activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating contitions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoletic disorders (e.g., wyploid or lymphoid or lymphoid call disease, haematopoletic disorders (e.g., wyploid or lymphoid or arthritis), arthritish partial isthermed therefore or arthritish proliferative retainpathy, atherosclerosis, coronary heart disease, arthritish partial isthermed. arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal vascular growth. Polypeptides involved with tissue regeneration and repair (or nucleic acids encoding them) may be used to promote wound healing (e.g., of burns, incisions and ulcers), while those with immunomodulatory activities may be used in the treatment of viral, bacterial and fungal infections in addition to immune disorders. Polypeptides with factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells

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that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a novel human polypeptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                22; Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64.9%; Score 37; DB 22; Length 517; 100.0%; Pred. No. 3e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster polypeptide SEQ ID NO 27267.
                                                                                                                             64.9%; Score 37; DB 66.7%; Pred. No. 89; iive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Myers EW;
                                                                                                                                                                                                                                                                                                   ABB66825 standard; Protein; 517 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                          Local Similarity 66.7
les 6; Conservative
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                                                                                                                                                                                                                       35 FLYVWGGYV 43
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Best Local Similarity
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                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                    ABB66825;
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us-09-870-089b-3.rag

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Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
vitamin B12; bacterial infection; disease.
                                                                                                      11-APR-2001; 2001WO-FR01118.
                                                                                                                           11-APR-2000; 2000FR-0004629.
                                         Listeria monocytogenes.
                                                                                                                                              (INSP ) INST PASTEUR
                                                              WO200177335-A2.
                                                                                   18-OCT-2001
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIGIT6-ABLIGOT1), expressed DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ABBS7737-ABB72072).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
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                                                                                                                                          Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
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                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 34164; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64.9%; Score 37; DB 22; Length 524; 100.0%; Pred. No. 3.1e+02;
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                                                                                                                       Drosophila melanogaster polypeptide SEQ ID NO 34164.
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                                                         ABB69124 standard; Protein; 524 AA.
                                                                                                                                                                                                                                                                                                                PWD,
                                                                                                                                                                                                                                       23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                            23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                   26-MAR-2002 (first entry)
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Matches 5; Conserv
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     505 YKWHG
                                                                                                                                                                                               WO200171042-A2
                                                                                                                                                     pharmaceutical
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                                                                              ABB69124;
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                                     RESULT 14
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Listeria monocytogenes protein #1833

05-FEB-2002 (first entry)

ABB49129

BXAXEXB

ABB40129 standard; Protein; 552 AA

RESULT 15

ABB49129

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The present invention relates to the genome sequence of Listeria

monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of
it are useful for selecting probes and primers for detecting genes in L.

compocytogenes and related organisms, and for studying genes in L.

monocytogenes and related organisms, and for studying genes in L.

compocytogenes and related organisms, and for studying genetic

compocytogenes and cher genomes. The present invention. Proteins

compocytogenes and proteins

compositions of L. monocytogenes and related organisms, and

compositions that regulate gene expression and cell replication

compocytogenes and proteins encoded by it are also useful for

sequence and proteins encoded by it are useful in pharmaceutical and

compocytogenes and related diseases. In addition, the genome

compocytogenes and related organisms.

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Cossart P;
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Buchrieser C, Frangeul L, Couve B, Rusniok C, Fsihi H, Dehoux P Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA, Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L, Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N, Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J,
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                                                                                                                                                                                                                                                                                                                                                                                                                          Genomic sequence for Listeria monocytogenes, useful e.g. for and prevention of Listeria and related bacterial infections,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 6; SEQ ID No 1834; 192pp; French.
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Pose M, Voss H;
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December 16, 2003, 14:11:00; Search time 12.3333 Seconds (without alignments) 30.875 Million cell updates/sec
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/cgn2 6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2 6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2 6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2 6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                      328717 seqs, 42310858 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                         seq length: 0
seq length: 200000000
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57
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 31268, A Sequence 28820, A Sequence 2, Appli Sequence 2, Appli Sequence 4341, Ap Sequence 6117, Ap Sequence 5771, Ap Sequence 5771, Ap Sequence 25679, A Sequence 222, App Sequence 222, App Sequence 222, App Sequence 219, App Sequence 99, Appl Sequence 91, Appl 185, App 222, App 219, App 182, App 89, Appl 90, Appl 91, Appl 92, Appl 90, Appl 91, Appl Sequence 13, Appl Sequence 330, App Sequence 2, Description Sequence Sequence Sequence Sequence US-09-073-009-13 US-09-216-393B-330 US-08-84-153-2 US-09-252-991A-2820 US-09-282-203-2 US-09-282-125A-2 US-09-282-125A-2 US-09-134-001C-4341 US-09-134-001C-4341 US-09-107-532A-6117 US-09-107-532A-6117 US-09-107-532A-6117 US-09-107-532A-6117 US-09-107-532A-6117 US-09-107-532A-6117 US-09-107-532A-6117 US-09-252-991A-2771 US-09-252-991A-2771 US-09-482-273-182 US-09-591-632-90 US-09-591-632-90 US-09-611-451-91 SUMMARIES BB Length Query Match 61.4 59.6 6.9 6.9 6.9 6.9 6.9 6.9 Score Result 80

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Gaps

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Score 36; DB 4; Length 144; Pred. No. 31; 1; Mismatches 2; Indels

63.2%; 62.5%;

Query Match 63.2 Best Local Similarity 62.5 Matches 5; Conservative

1 FLYKWHGF 8

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Mycobacterium tuberculosis

ORGANISM: US-09-073-009-13

LENGTH: 144 amino acids TYPE: amino acid STRANDEDNESS: single

single

TOPOLOGY: linear MOLECULE TYPE: peptide ORIGINAL SOURCE:

Sequence 92, Appl Sequence 183, App Sequence 120, App Sequence 119, App Sequence 38, Appl Sequence 4, Appl Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 1, Appli Sequence 1865, A Sequence 1865, A Sequence 1855, Appli Sequence 1855, Appli Sequence 1855, Appli Sequence 35, Appli Sequence	TUBERCULOSIS AND M	
4 US-09-611-451-92 4 US-09-482-273-183 4 US-09-482-273-220 4 US-09-482-273-120 4 US-09-328-352-5216 4 US-09-328-352-5216 4 US-09-328-352-5216 2 US-08-663-56A-4 2 US-08-663-66A-4 2 US-08-23-610-4 3 US-08-286-055A-4 4 US-09-252-991A-19865 4 US-09-134-010C-4435 US-09-252-991A-19865 4 US-09-134-01C-4435 US-09-285-957-35	ALIGNMENTS 1 US/09073009 Mark Aavin C. fasir A.W. tc, Antonio COMPOUNDS AND DIAGNOSIS OF 144 S.S. S.S. S.S. S.S. S.S. S.	WH: Y disk Compatible Compatible Solve ALTA: US/09/073,009 W-1998 ALTON: US. 1392 ALTON: US. 1393 ALTON: US.
33 57.9 128 139 139 139 139 139 139 139 139	pplication 5653 MATION: MATION: Dillon, I Skeiky, N CARTION: EQUENCES: NCE ADDRES: NCE ADDRES: SEED at 16	ZIP: 9810A ZIP: 9810A MEDIUM TYPE: FLORDY disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS SOFTWARE: PACENTIN RELEASE CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/0 FILING DATE: 05-MAY-1998 CLASSIFICATION: NAME: MAXI, DAVIG J. REGISTRATION: NAME: MAXI, DAVIG J. REGISTRATION NUMBER: 31,392 REFERENCE/DOCKET NUMBER: 21 TELECOMMUNICATION INPORMATION: TELEPHONE: 206-622-4900 TELEPHONE: 206-6310101111111111111111111111111111111
00000000000000000000000000000000000000	RESULT 1 US-09-073-009-13 Sequence 13, A Petent No. 655 GENERAL INFOR APPLICANT: APPLICA	CON CONTRACTOR OF CONTRACTOR O

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Sequence 28820, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION NUMBER: US/09/252,991A
FILE REPRENCE: 107196.136
CURRENT APLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 28820
LENGTH: 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: ALRUCIEC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 31268
LENGTH: 453
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                                                                                                                              63.2%; Score 36; DB 2; Length 348; 62.5%; Pred. No. 77;
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Pred. No. 1e+02;
2; Mismatches 2; Indels
                                                                                                                                                                                             1; Mismatches
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ORGANISM: Pseudomonas aeruginosa
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55.6%;
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                                 MOLECULE TYPE: protein
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   TOPOLOGY: linear
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US-08-844-153-2
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                                                                                                                                                 % Sequence 330, Application US/09216393B

% Sequence 330, Application US/09216393B

% Sequence 330, Application US/09216393B

% Datent No. 6514694

% GENERAL INFORMATION:
% APPLICATION
TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USES THER
% TILLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USES THER
% FILE REFERENCE: TX-1-C2
% CURRENT FILING DATE: 1998-12-18
% PRIOR PILING DATE: 1997-12-19
% PRIOR PILING DATE: 1997-12-19
% PRIOR PILING DATE: 1997-12-19
% NUMBER OF SEQ ID NOS: 366
% SOFTWARE: Patentin version 3.1
% SEQ ID NO 330
% TOXOPL. 10-7
% TO
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Pred. No. 43;
1; Mismatches 1; Indels
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SOFTWARE: FastSEC for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/844,153
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9607992.6
ATTORNEY, AGENT INPORMATION:
NAWE: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REGISTRATION NUMBER: 38,891
REGISTRATION NUMBER: 38,891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Lawlor, Elizabeth
TITLE OF INVENTION: No. 5958734el Compounds
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08844153
Patent No. 5958734
GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 2:
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TELEFAX: 610-270-5090
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LENGTH: 348 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Toxoplasma gondii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 71.4
Matches 5; Conservative
| | | | :
134 FLCSWHGY 141
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Gaps
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                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 8
US-09-273-142-2
Sequence 2, Application US/09273142
Patent No. 6300119
GENERAL INFORMATION:
APPLICANT: Jaworski, Deborah
APPLICANT: Lawlor, Elizabeth
APPLICANT: Wang, Min
TILE OF INVENTION: NOVEL STREPTOCOCCAL ERS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSE: SMITHKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63.2%; Score 36; DB 3; 3 62.5%; Pred. No. 1.1e+02; tive 1; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIF: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FESTESC for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/273,142
                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/962,203
FILING DATE: «UAKNOWN»
APPLICATION NUMBER: 9607992.6
FILING DATE: 18-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P31459-1
TELECOMMUNICATION INFORMATION:
TELEFONE: 610-270-4478
                                                                                                            SOFTWARE: FASTOLY
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/282,125A
FILING DATE: 07-Aug-2000
CLASSIFICATION: <UNKNOWN>
18-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 480 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-APR-1996
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 62.5
Matches 5; Conservative
COUNTRY: USA
ZIP: 19406-0939
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 LYKWHGFV 9
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                                                                                                                                                                                                                                                                                                                         COMPUREY: PA

COMPUTER: USA

ZIP: 19406-0939

COMPUTER READABLE FORM:
MEDIUM TYBE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTESO for Windows Version 2.0
SOFTWARE: 10508/962,203
FILING DATE: 31-02T-1997
FILING DATE: 31-02T-1997
FILING DATE: 18-APR-1997
FILING DATE: 18-APR-1997
APPLICATION NUMBER: 08/844,153
FILING DATE: 18-APR-1997
APPLICATION NUMBER: 9607992.6
FILING DATE: 18-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, ZGWARG
REFERENCE/DOCKET NUMBER: 38,891
REFERENCE/DOCKET NUMBER: 38,991
REFERENCE/DOCKET NUMBER: 931459-1
                                        Sequence 2, Application US/08962203;
Patent No. 5976840
GENERAL INFORMATION:
APPLICANT: Jawnorski, Deborah
APPLICANT: Lawlor, Elizabeth
APPLICANT: Wang, Min
TITLE OF INVENTION: NOVEL STREPTOCOCCAL ERS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STAME: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Jaworski, Deborah
Lawlor, Elizabeth
Wang, Min
TITLE OF INVENTION: NOVEL STREPTOCOCCAL ERS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/09282125A Patent No. 6165760 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 480 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TONOLOGY: linear; MOLECULE TYPE: protein US-08-962-203-2
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159 IYKWHDMV 166
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                               US-08-962-203-2
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APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                                                                                                                                   Length 351;
                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                 61.4%; Score 35; DB 4; L. 100.0%; Pred. No. 1.2e+02; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 35; DB 4; ]
Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION UNMERS: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION UNMERS: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) NAME/KEY: misc_feature
; LOCATION: (B) LÖCATION 1...472
; SEQUENCE DESCRIPTION: SEQ ID NO: 6117:
US-09-107-532A-6117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INCOMATION:
NAME: Arinfello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6117, Application US/09107532A Patent No. 6583275 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: PC
OPERATING SYSTEM: <Unknown>
CURRENT FILING DATE: 2000-08-04
PRIOR APPLICATION WUMBER: 60/147,164
PRIOR FILING DATE: 1999-08-04
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 11
LENGTH: 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 472 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 6117:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                        TYPE: PRT
ORGANISM: Bordetella pertussis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: ASCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Waltham
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                    105 WHGFV 109
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                                                                                                                                                                                                       US-09-632-947B-11
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Patent No. 6380370

Patent No. 6380370

Patent No. 6380370

APPLICANT: INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
FILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT APPLICATION NUMBER: US 60/064,964

PRIOR PAPLICATION NUMBER: US 60/064,964

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR APPLICATION NUMBER: US 60/055,779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11, Application US/09632947B

Patent No. 6556845

GENERAL INCORMATION:
APPLICANT: Pharmacia & Upjohn

TITLE OF INVENTION: CRYSTALLIZATION AND STRUCTURE DETERMINATION OF

TITLE OF INVENTION: UDP-N-ACETYLENOLPYRUVYLGLUCOSAMINE REDUCTASE (S. aureus
TITLE OF INVENTION: MAID)

FILE REFERENCE: 268.6241 0101

CURRENT APPLICATION NUMBER: US/09/632,947B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 36; DB 4; Length 480
Pred. No. 1.1e+02;
1; Mismatches 2; Indels
                                                                                                                                                          P31459-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Staphylococcus epidermidis
  APPLICATION NUMBER: 08/962,203
                FILING DATE:
MAPELING DATE:
FILING DATE:
18-APR-1990.6
FILING DATE:
18-APR-1990.8
ATTORNEY/AGENT INFORMATION:
NAME:
REGISTRATION NUMBER:
TELECHONICATION INFORMATION:
TELECHONE: 610-270-4478
                                          9607992.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63.2%;
                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH. 480 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       159 IYKWHDMV 166
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Best Local Similarity
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Best Local Similarity
Matches 5; Conserv
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Sequence 5771, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03P8. US/09/328,352
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-66-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 5771
LENGTH: 539
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-07-18
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 25679
LENGTH: 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-07-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
LENGTH: 629
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Pred. No. 2.7e+02;
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Pred. No. 2.2e+02;
1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5771
                                                                                                                                                                                                          TYPE: PRT ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31575
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Best Local Similarity 80.0
Matches 4; Conservative
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Best Local Similarity 80.0
Matches 4; Conservative
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79 WHGFI 83
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US-09-252-991A-31575
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ORGANISM:
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 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
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; LOCATION: (B) LOCATION 1...257
; SEQUENCE DESCRIPTION: SEQ ID NO: 5440:
US-09-107-532A-5440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: GTC-012 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 25679, Application US/09252991A
Parent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
                                                                                                                                                                                                                                                                                                                                                                    ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                   STREET: 100 Beaver Street
CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (781)893-5007
TELEPK: (781)893-8277
INFORMATION FOR SEQ ID NO: 5440:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 257 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                      STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
 4; Conservative
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183 YLYRWH 188
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Best Local Similarity
Matches 4; Conserv
                               1 FLYKWH 6
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11 YLFKWH 16
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ö 0; Gaps Query Match 59.6%; Score 34; DB 4; Length 629; Best Local Similarity 80.0%; Pred. No. 3.1e+02; Matches 4; Conservative 1; Mismatches 0; Indels

5 WHGFV 9 ||||: 172 WHGFI 176

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Search completed: December 16, 2003, 14:20:39 Job time: 13.333 secs

Sequence 5, Appli Sequence 12, Appl Sequence 13, Appl Sequence 11, Appl Sequence 10326, A Sequence 10326, A Sequence 10326, A Sequence 1256, Ap Sequence 1756, Ap Sequence 1776, Ap Sequence 1776, Ap Sequence 1706, Ap Sequence 11, Appl Sequence 1108, A Sequence 1108, A Sequence 111, Appl Sequence 111, Appl Sequence 111, Appl Sequence 11, Appl Sequence 21, Appl

Sequence Sequence

```
Sequence 3, Application US/09870089B
Publication No. US20030175252A1
GENERAL INFORMATION:
APPLICANT: Charles A. Nicolette
TITLE OF INVENTION: THERAPEUTC COMPOUNDS FOR OVARIAN CANCER
FILE REPREND. 68126881208700
CURRENT APPLICATION NUMBER: US/09/870,089B
CURRENT FILING DATE: 2001-05-30
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FASTSEO FOR Windows Version 3.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9, Application US/09870089B
; Publication No. US20030175252A1
; GENERAL INFORMATION:
    APPLICANT: Charles A. Nicolette
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS FOR OVARIAN CANCER
; FILE REFERENCE: 68126881209900
; CURRENT APPLICATION NUMBER: US/09/870,089B
| US-10-203-224-5 | US-10-403-224-5 | US-10-9443-704-12 | US-10-166-225A-53 | US-10-166-225A-53 | US-10-166-225A-53 | US-10-166-225A-53 | US-10-166-225A-53 | US-10-166-226 | US-10-166-761-828 | US-10-166-761-828 | US-10-166-761-1036 | US-10-169-71-27 | US-10-169-71-266 | US-10-189-437-565 | US-10-199-437-565 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 57; DB 12;
100.0%; Pred. No. 6.1e+05;
ttive 0; Mismatches 0;
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US-09-970-0898-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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Matches 9; Conservative
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     Query Match
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Sequence 19, Appli
Sequence 19, Appli
Sequence 7, Appli
Sequence 13, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 130, App
Sequence 130, App
Sequence 1365, Ap
Sequence 1180, Ap
Sequence 1180, Ap
                                                                                                                          December 16, 2003, 14:18:11; Search time 22.1667 Seconds (without alignments) 75.512 Million cell updates/sec
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18: /cgn2_6/ptodata/2/pubpaa/USO0B_PUBCOMB.pep:*
                 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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2 US-09-870-089B-9

1 US-09-791-279-198

1 US-09-791-279-198

US-09-073-009-13

US-09-073-009-13

US-09-073-306-13

US-09-793-306-13

US-09-793-306-13

US-09-158-1330

US-09-168-13455

US-09-815-242-13455

US-09-815-242-13455

US-09-815-242-13455

US-09-815-248-12

US-09-815-248-12

US-09-815-248-12

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Maximum Match 1008
Listing first 45 summaries
                                                                                          - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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57
1 FLYKWHGFV 9
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Match Length
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US-09-870-089B-7
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                                                                                                                                                                                                                                                                                                                                                                          Score 41; DB 12; Length 9;
Pred. No. 6.1e+05;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THILD OF INVESTION: NO. US20030050456A1E1 (FILE REFERENCE: 00048.US1 (CURRENT APPLICATION WUMBER: US/09/791,279 (CURRENT FILING DATE: 2001-02-23 (PRIOR FILING DATE: 2000-02-24 (PRIOR APPLICATION NUMBER: 60/184,716 (PRIOR FILING DATE: 2000-02-24 (PRIOR FILING) PRIOR FILING PRIOR FILING PRIOR FILING PRIOR FILING PRIOR FILING PRIOR FILING PRI
CURRENT FILING DATE: 2001-05-30
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 9
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 198, Application US/09791279
Publication No. US20030050456Al
GENERAL INFORMATION:
                                                                                                                                                                                                                                   FEATURE:
CTHER INFORMATION: ATF4/CREB-2
US-09-870-089B-9
                                                                                                                                                                          TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                              71.9%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Vogeli, Gabriel
APPLICANT: Wood, Linda S.
APPLICANT: Parodi, Luis
APPLICANT: Lind, Peter
                                                                                                                                                                                                                                                                                                                                                                       Query Match 71.9
Best Local Similarity 66.7
Matches 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              || ||||
84 FLNLWHGFL 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 FLYKWHGFV 9
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1 FLHKWHWYV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 FLYKWHGFV 9
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LENGTH: 220
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RESULT

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APPLICANT: Ruben et al.

TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
FILE REPRENCE: PAGOSPI.

CURRENT APPLICATION NUMBER: US/10/106,698

CURRENT FILING DATE: 2002-03-27

RIOR APPLICATION NUMBER: PCT/US00/26524

PRIOR APPLICATION NUMBER: PC 60/157,137

PRIOR APPLICATION NUMBER: US 60/157,137

PRIOR PILING DATE: 1999-09-29

PRIOR PILING DATE: 1999-01-03

NUMBER OF SEQ 1D NOS: 8564

SOFTWARE: Patentin Ver: 3.0

SEQ 1D NO 5220

LENGTH: 92
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Sequence 7, Application US/09870089B; Publication No. US20030175252A1; Publication No. US20030175252A1; General Information:
GENERAL INFORMATION:
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS FOR OVARIAN CANCER; TITLE OF INVENTION: WIMPARTION OF SEQUENCE: 68126881209900; CURRENT FILING DATE: 2001-05-30; NUMBER OF SEQ ID NOS: 14; SOFTWARE PREFECT FRANCE.
SEQ ID NO 7

LENGTH: 9
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                                                                                                                                                                                                                                                                                                                                                                                                               Score 37; DB 12; Length 9;
Pred. No. 6.1e+05;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    Length 9;
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Patent No. US20010012888A1
GENERAL INFORMATION:
APPLICANT: Alderson, Mark
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Campos-Neto, Antonio
TITLE OF INVENTION: COMPOUNDS AND DIAGNOSIS OF
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-106-698-5220
; Sequence 5220, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                              CTHER INFORMATION: ATF4/CREB-2
US-09-870-0898-7
                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                  64.9%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 66.7
Matches 6; Conservative
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Best Local Similarity 71.4
Matches 5; Conservative
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US-10-106-698-5220
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LFKWHNF 12
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APPLICANT: Skelky, Yasir
APPLICANT: Ovendale, Pamela
APPLICANT: Ovendale, Pamela
APPLICANT: Ovendale, Pamela
APPLICANT: Ucdes, Michael
APPLICANT: Ucdes, Michael
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compounds and Methods for Diagnosis and Immunotherapy
TITLE OF INVENTION: Of Tuberculosis
FILE REFERENCE: 014058-008740US
FILE REFERENCE: 014058-008-02-25
FRIOR APPLICATION NUMBER: US 60/223,828
FRIOR APPLICATION NUMBER: US 60/223,828
FRIOR PRING DATE: 2000-08-08
NUMBER OF SEQ ID NOS: 164
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 330, Application US/09216393
Patent No. US2001001447A1
GENERAL INFORMATION:
APPLICANT: Milhausen, Michael James
TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND
                                                                                                                                                                                                                                                                                  63.2%; Score 36; DB 9; Length 144; 62.5%; Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63.2%; Score 36; DB 9; Length 144; 62.5%; Pred. No. 1.5e+02; 1ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                               TOPOLOGY: linear MolECULE TYPE: peptide
CORGINAL SOURCE:
CREANISM: Mycobacterium tuberculosis
US-09-023-588-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: MOD_RES

// LOCATION: (1)...(144)

OTHER INFORMATION: Xaa = any amino acid
US-09-793-306-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13, Application US/09793306
Patent No. US200200098200A1
GENERAL INFORMATION:
APPLICANT: Campos-Neto, Antonio
             TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
(206) 622-4900
                                                                               LENGTH: 144 amino acids
TYPE: amino acid
STRANDEDNESS: Bingle
TOPOLOGY: linear
                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Tb224
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                                                                                                                                                                                                                                                                                                                                                                                                               134 FLCSWHGY 141
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US-09-216-393-330
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US-09-793-306-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
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                                                                                           COMPUTER READABLE FORM:

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FOC. COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,009
FILING DATE: 05-MAY-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, DAY'd J.
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 210121.441C1
TELECOMMUNICATION:
TELEPHONE: 206-622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 98104
COMPUTER READABLE FORM:
MEDTING TYPE: Floppy disk
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,588
FILING DATE: 14-FEB-1998
CLASSIFICATION:
E: SEED and BERRY
6300 Coumbia Center, 701 Fifth Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.445
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 206-682-6031
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 144 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 63.2
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         || |||:
134 FLCSWHGY 141
                                    Seattle
Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 FLYKWHGF 8
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US-09-023-588-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-073-009-13
                                                                                  COUNTRY:
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LOCATION: (42)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (75)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: SITE
LOCATION: (81)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . LOCATION: (95)
. OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-925-299-1180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (89)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1180, Application US/09925299;
Fatent No. US20020055627A1;
GENERAL INFORMATION:
TITLE OF INFORMATION:
TITLE OF INFORMATION:
CURRENT APPLICATION NUCLEIC Acids, Proteins and Antibodies;
CURRENT APPLICATION NUMBER: US/09/925,299;
CURRENT FILING DATE: 2001-08-10;
FRIOR PELING DATE: 2001-08-10;
FRIOR APPLICATION NUMBER: FCT/US00/05883;
FRIOR APPLICATION NUMBER: 60/124,270;
FRIOR APPLICATION NUMBER: 60/124,270;
FRIOR PILING DATE: 1999-03-12;
NUMBER OF SEQ ID NOS: 1556;
SOFTWARE: Patentin Ver. 2.0;
LENGTH: 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 36; DB 9; Length 486; Pred. No. 4.5e+02; Indels 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61.4%; Score 35; DB 9; Length 96; 83.3%; Pred. No. 1.5e+02; ive 0; Mismatches 1; Indels
                    PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-110-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR PRILING DATE: 2001-12-22
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: PASTESEQ FOR WINDOWS VERSION 4.0
SEQ ID NOS: 14110
                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Streptococcus pneumoniae US-09-815-242-13455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 62.5%;
Matches 5; Conservative
       FILING DATE: 2000-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 83.3
Matches 5; Conservative
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165 IYKWHDMV 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 LYKWHGFV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-925-299-1180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Milhausen, Michael James
TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USES THER
FILE REPERENCE: TX.1-C2.1
CURRENT APPLICATION NUMBER: US/10/321,856
CURRENT FILING DATE: 2002-12-17
PRIOR APPLICATION NUMBER: 09/216,393
PRIOR APPLICATION NUMBER: 09/216,393
PRIOR APPLICATION NUMBER: 09/94,825
PRIOR APPLICATION NUMBER: 09/94,825
PRIOR RILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 366
SOFTWARE: Patentin version 3.1
SEQ ID NO 330
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Pred. No. 2e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Oblisen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Tranick, John D.
APPLICANT: Tranick, John D.
APPLICANT: Tranick, John D.
APPLICANT: Yanamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
TITLE OF INVENTION: Prokaryotes
TITLE OF INVENTION: 10011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
                                                                                                                                                                                                                                                                                              Score 36; DB 9; Length 197;
Pred. No. 2e+02;
1; Mismatches 1; Indels
CURRENT APPLICATION NUMBER: US/09/216,393
CURRENT FILING DATE: 1998-12-18
EARLIER APPLICATION NUMBER: 08/994,825
EARLIER FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 364
SOFTWARE: PatentIn Ver. 2.0
ERQ ID 10 330
LENGTH: 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13455, Application US/09815242 Patent No. US20020061569Al GENERAL INFORMATION: APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
US-10-321-856-330
; Sequence 330, Application US/10321856
; Publication No. US20030194393A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Toxoplasma gondii
US-10-321-856-330
                                                                                                                                                                                                    TYPE: PRT; ORGANISM: Toxoplasma gondii
US-09-216-393-330
                                                                                                                                                                                                                                                                                                                                                                                                                                  173 LLRWHGF 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               173 LLRWHGF 179
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Query Match 61.4%; Score 35; DB 9; Length 99; Best Local Similarity 75.0%; Pred. No. 1.6e+02; Matches 6; Conservative 0; Mismatches 2; Indels
  ; ORGANISM: Drosophila sp. US-09-815-248-12
                                                                                                                                                                                                    13 LYIWHKFV 20
                                                                                                                                                          2 LYKWHGFV 9
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140 MYQWHG 145
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                                                                                                                                                                                                                                                                   RESULT 15
US-10-407-079-109
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Patent No. US20020098540a1
GENERAL INFORMATION:
APPLICANT: RASTELL, LUCA
APPLICANT: PENNICA, DIANE
TITLE OF INVENTION: NOVEL POLYPEPTIDES, AND NUCLEIC ACIDS ENCODING THE SAME
FILE REFERENCE: 10716.36
CURRENT FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: 60/191,258
PRIOR FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 12
LENGTH: 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRATURE:
NAME/KEY: SITE

LOCATION: (42)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
LOCATION: (50)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
LOCATION: (50)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
LOCATION: (75)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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Publication No. US20030040617A9
GENERAL INFORMATION:
APPLICANT: ROSen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: ECT/US00/05883
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 180
LENGTH: 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61.4%; Score 35; DB 11; Length 96, 83.3%; Pred. No. 1.5e+02;
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 5; Conserr
                                       69 YKWQGF 74
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3 YKWHGF 8
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US-09-815-248-12
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APPLICANT: Glucksmann, Maria A. APPLICANT: Carroll, Joseph M. APPLICANT: Carroll, Joseph M. APPLICANT: Galvin, Katherine M. TITLE OF INVENTION: 45449, 50289, 52872 AND 265908 MOLECULES AND USES THEREFOR FILE OF INVENTION: 45449, 50289, 52872 AND 265908 MOLECULES AND USES THEREFOR JUNEBRY APPLICANTON NUMBER: US 10/226,102 PRIOR APPLICANTON NUMBER: US 10/226,102 PRIOR APPLICANTON NUMBER: US 60/314,041 PRIOR APPLICANTON NUMBER: US 60/314,185 PRIOR FILING DATE: 2002-08-22 PRIOR FILING DATE: 2001-08-22 PRIOR FILING DATE: 2001-08-22 PRIOR FILING DATE: 2001-08-22 PRIOR FILING DATE: 2001-08-22 PRIOR FILING DATE: 2002-10-15 PRIOR APPLICANTON NUMBER: US 60/314,185 PRIOR APPLICANTON NUMBER: US 60/314,185 PRIOR FILING DATE: 2000-11-17 PRIOR APPLICANTON NUMBER: US 60/19,845 PRIOR FILING DATE: 2000-11-17 PRIOR APPLICANTON NUMBER: US 60/19,845 PRIOR FILING DATE: 2000-10-24 PRIOR FILING DATE: 2000-02-24 PRIOR FILING DATE: 2000-02-29 PRIOR FILING DATE: 2000-02-24 PRIOR DATE: 2000-02-24 PRIOR PR
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                                                                                                                                                           APPLICANT: Millennium Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: December 16, 2003, 14:41:05 Job time: 22.1667 secs
Sequence 109, Application US/10407079
Publication No. US20030215860A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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           kluyveromyc
escherichia
                                                                                   bacillus su
spinacia ol
dictyosteli
                                homo sapien
                                           mus musculu
                                                                pseudomonas
                                                                                                                     epstein-bar
                                                      rattus norv
                                                                          arbacia lix
                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic Acids Res. 24:4420-4449(1996).
-1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MSBA SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                        "Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, AE000015; AAB95783.1; -.

R PIR; S73461; S73461.

R InterPro; PR003593; AAA ATPase.
R InterPro; IPR003593; AAA ATPase.
R InterPro; IPR003439; ABC_TM_transpt.
R InterPro; IPR003439; ABC_transporter.
Pfam; PF00066; ABC_transporter.
R ProDom; PD000006; ABC_transporter; 1.
R PROSITE; PS0031; AAA; 1.
R PROSITE; PS0031; AAA; 1.
R PROSITE; PS0031; AAA; 1.
R PROSITE; PS0031; ABC_TRANSPORTER 1; 1.
R PROSITE; PS0031; ATP-binding; Transmembrane; Complete proteome.
R TRANSMEM 111 131 POTENTIAL.
                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical ABC transporter ATP-binding protein MG015 homolog
                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma
NCBL_TaxID=2104;
                              075712
P28231
P25305
Q51548
P34941
006005 1
Q9sek3
P36418 C
           O60014
P76363
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=ATCC 23342 / M129;
MEDLINE=97105885; PubMeg-8948633;
Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FP (POTENTIAL).
E10CE07E0EBBD406 CRC64;
                                                                                                                                                    ALIGNMENTS
 HCYC EURCA
UBRI KLUIA
YEET ECCLI
CXR3 HUMAN
CXR3 MOUSE
CXR3 RAT
PUDA ARBLI
NU4M ARBLI
AARA BACSU
AARA BACSU
VIXI SPIOL
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  (D12 orf634).
MPN019 OR MP135.
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ID YO15 MYCPN
AC P75094;
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                                                                     December 16, 2003, 14:06:35; Search time 5.6667 Seconds (without alignments) 74.689 Million cell updates/sec
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P57490 ]
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Q8dzr1
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Q8dvx9
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P80476
Q9nfh9
        GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                         127863 segs, 47026705 residues
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GSPF_PSEAE
MTX2_XANOR
SYE_STRMU
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SYE STRNU
SYE STRPN
SYE STRPN
SYE STRN
YOUG CAREL
HOYG ENCA
DCOR ECOLI
YJ9G YEAST
YRVH ECOLI
LSPA ECOSI
LSPA ECOSI
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ADVI MOUSE
SYQ BUCAI
YO15 MYCGE
SYW PYRAE
CCS CITSI
G6PD DROYA
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Maximum DB seq length: 2000000000
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                                                                                                              US-09-870-089B-3
57
1 FLYKWHGFV 9
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Match Length DB
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SYQ BUCAI
P57490;
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SEQUENCE
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- TISSUE SPECIFICITY: MOST HIGHLY EXPRESSED IN THE ENDOMETRIUM OF THE UTERUS, THE INTESTINAL VILLI AND THE TEGTES. WEAKER EXPRESSION ALSO DETECTED IN THE BRAIN AND ON THE SURFACE OF THE TONGUE.

-i- DEVELOPMENTAL STAGE: HIGHEST EXPRESSION WAS DETECTED IN DORSAL ROOT AND TRIGEMINAL GANGLIA BY EMBRYONIC DAY 14.5 AND CONTINUED THROUGH AT LEAST DAY 16.5.

-i- SIMILARITY: BELONGS TO THE VILLIN/GELSOLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=NIH Swiss;
MEDLINE=98315054; PubMed=9649432;
MEDLINE=98315054; PubMed=9649432;
Mang X.-Z., Kuroda M., Sok J., Batchvarova N., Kimmel R., Chung P.,
Zinszner H., Ron D.;
"Identification of novel stress-induced genes downstream of chop.";
EMBO J. 17:5619-3630 (1998).
-!- FUNCTION: CA.(2+) - REGULATED ACTIN-BINDING PROTEIN. MAY HAVE A
-!- FUNCTION: CA.(2+) - REGULATED ACTIN-BINDING PROTEIN. MAY HAVE A
-!- UNIQUE PUNCTION IN THE MORPHOGENESIS OF NEURONAL CELLS WHICH FORM
                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=BALB/c; TISSUE=Brain;
MEDLINE=98330437; PubMed=5664034;
Marks P.W., Arai M., Bandura J.L., Kwiatkowski D.J.;
Mayillin (p92): a new member of the gelsolin/villin family of actin regulatory proteins.";
                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRODS97; GELSOLIN.
SMART; SM00262; GEL; 6.
SMART; SM00153; VHP; 1.
Cytoskeleton; Calcium; Actin-binding; Capping protein; Repeat.
DOMAIN 732 819 HEADPIECE (BY SIMILARITY).
70.2%; Score 40; DB 1; Length 634; 55.6%; Pred. No. 13; ive 2; Mismatches 2; Indels
                                                                                                                                                                               ADVL_MOUSE STANDARD; PRT; 819 AA. 088398; O70466; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 18-ERE-2003 (Rel. 41, Last annotation update) Advillin (p92) (Actin-binding protein DOC6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; PO2640; ZVIL.
MGD; MG1:1333798; Avil.
Oct G0:0006950; P:response to stress; IDA.
InterPro; IPR001974; Gelsolin.
InterPro; IPR0013128; VHP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     regulatory proteins.";
J. Cell Sci. 111:2129-2136(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF041448; AAC25050.1; -. EMBL; AF059486; AAC31808.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00626; Gelsolin; 6.
Pfam; PF02209; VHP; 1.
                 Best Local Similarity 55.6
Matches 5; Conservative
                                                                                      297 FIXSWEGFI 305
                                                                   1 FLYKWHGFV 9
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                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
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   Query Match
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MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GLNS OR BU415.
Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FIRAIN=TOKYO 1998;
MEDLINE=20445173; PubMed=10993077;
MEDLINE=20445173; PubMed=10993077;
Matanabe H., Hattori M., Sakaki Y., Ishikawa H.;
"Genome sequence of the endocellular bacterial symbiont of aphids
Buchmera sp. APS.";
Nature 407:81-86(2000).
-!- CATALYTIC ACTIVITY: ATP + L-glutamine + tRNA(Gln) = AMP +
dlphosphate + L-glutaminyl-tRNA(Gln).
-!- GATALYTIC MORDER (By similarity).
-!- SUBUNIT: MORDER (Sy similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2003 (Rel. 41, Last annotation update)
Glutaminyl-tRNA synthetase (EC 6.1.1.18) (Glutamine--tRNA ligase)
(GlnRS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Buchnera.
                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                 POLYPHOSPHOINOSITIDE BINDING (BY SIMILARITY).
                                                                                                                     POLYPHOSPHOINOSITIDE BINDING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                         Query Match 68.4%; Score 39; DB 1; Length 819; Best Local Similarity 83.3%; Pred. No. 25; Matches 5; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                   R -> G (IN REF. 2).
R -> G (IN REF. 2).
I -> N (IN REF. 2).
R -> Q (IN REF. 2).
R -> X (IN REF. 2).
R -> K (IN REF. 2).
W, 88CD9DBDEDFIF77D CRC64;
GELSOLIN-LIKE 1
GELSOLIN-LIKE 2
GELSOLIN-LIKE 3
GELSOLIN-LIKE 4
GELSOLIN-LIKE 5
GELSOLIN-LIKE 5
VHP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HAMAP; MF_00126; -; 1.
InterPro; IPR004514; 0.1nS.
InterPro; IPR00924; Glu ERNA-synt_1c.
InterPro; IPR001412; ERNĀ-synt_1c.
Pfam; PF00749; ERNA-synt_1.
Pfam; PF007950; ERNA-synt_1c.
PRINTS; PR00987; TRNA-SYNTHGIU.
                                                                                                                                                                                                                                                                          92186 MW;
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 73
185
306
454
565
669
819
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469
538
809
814
819 AA;
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                                                                                                                                                                                                                                                                                                                                                                            3 YKWHGF 8
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aerophilum.";
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    TRANSMEM
NP BIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The minimal gene complement of Mycoplasma genitalium.";
Science 270:397-403 (1995).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MSBA SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A., Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M., Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Puhrmann J.L., Wiguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M. Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S., Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
TIGRFAMs; TIGR00440; glnS; 1.
PROSITE; PS00178; AA TRNA LIGASE I; 1.
Aminoacyl-tRNA synthetase; Proteïn biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                             Gaps
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SWART; SM0382; AAA; 1.
PROSITE; PS00211; ABC TRANSPORTER 1; 1.
PROSITE; PS50893; ABC TRANSPORTER 2; 1.
Hypothetical protein; ATP-binding; Transport; Transmembrane;
                                                                                                                                                                                             Score 38; DB 1; Length 571; Pred. No. 26;
                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last amnotation update)
Hypothetical ABC transporter ATP-binding protein MG015.
                                                                                                         "KMSKS" REGION.
ATP (BY SIMILARITY).
1FCE69932D563D52 CRC64;
                                                                                                                                                                                                                                           0; Mismatches
                                                                                         "HIGH" REGION
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InterPro; IPR003593; AAA ATPase.
InterPro; IPR001140; ABC_TW transpt.
InterPro; IPR003439; ABC_transporter.
Pfam; PF00664; ABC_membrane; 1.
Pfam; PF00005; ABC_tran; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=ATCC 33530 / G-37;
MEDLINE=96026346; Pubmed=7569993;
                                                                                                                                                      571 AA; 67835 MW;
                                                                                                                                                                                                66.7%;
85.7%;
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                                                                                                                                                                                                                                         6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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273
272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycoplasma genitalium.
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                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                      3 YKWHGFV 9
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                                                                    Complete proteome.
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TRANSMEM 9
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269
272
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01-FEB-1996 (
16-OCT-2001 (
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                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
-!- CATALYTIC ACTYUTY: ATP + L-tryptophan + tRNA(Trp) = AMP + diphosphate + L-tryptophanyl-tRNA(Trp).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
Typtophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophan--tRNA ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
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                                                                                                    Score 38; DB 1; Length 589;
Pred. No. 27;
2; Mismatches 2; Indels
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POTENTIAL.
ATP (POTENTIAL).
0EA6A816DD3A3CC9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pyrobaculum aerophilum.
Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
Thermoproteaceae; Pyrobaculum.
NCBI_TaxID=13773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      262 "KMSKS" REGION.
43178 MW; 3DDBF85DA680F116 CRC64;
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InterPro; IPR0012105; tRNA-synt_lb.
InterPro; IPR001412; tRNA-synt_l.
InterPro; IPR002306; Trp_tRNA-synt_lb.
Pfam; PF00579; tRNA-synt_lb; 1.
PRINTS; PR01039; TRNA-SYNTHTRP.
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PROSITE; PS00178; AA TRNA LIGASE I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=IM2 / ATCC 51768 / DSM 7523,
MEDLINE=21664397; PubMed=11792869;
                                                66126 MW;
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                                                                                                    66.7%;
55.6%;
                                                                         Ouery Match
Best Local Similarity 55.0
5. Conservative
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les 5; Conservative
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323
392
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303
385
589 AA;
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SITE
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Xu C.J., Chen D.M., Zhang S.L.;
"Molecular cloning of capsanthin/capsorubin synthase gene from orange (Cittus sinensis).";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: CATALYZES THE CONVERSION OF THE UBIQUITOUS 5,6-
EPOXYCAROTENOIDS, ANTHERAXANTHIN AND VIOLAXANTHIN, INTO CAPSANTHIN
AND CAPSORUBIN, RESPECTIVELY.
                                                                                                                                                                                                                                                                                                                                                                                           3 YKWHGFV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                Transit peptide
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G6PD_DROYA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Citrus sinensis (Sweet orange).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots, Rosidae;
eurosids II; Sapindales; Rutaceae; Citrus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                01-NOV-1997 (Rel. 35, Created)
1-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable succinate-semialdehyde dehydrogenase [NADP+] (EC 1.2.1.16)
                                                                                                                                                                                                             MEDLINE-97305956; PubMed-9163424;
Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
Perret X.;
                                                                                                                                                                                                                                                              Nature 387:394-401(1997).
-!- CATALYTIC ACTIVITY: Succinate semialdehyde + NAD(P)(+) + H(2)O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
0
                                                                                                                                                                                                                                                  "Molecular basis of symbiosis between Rhizobium and legumes.";
                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: Belongs to the aldehyde dehydrogenase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NADP (ADP PART) (BY SIMILARITY).
                                                                                                                                    Plasmid sym pNGR234a.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64.9%; Score 37; DB 1; Length 491; 62.5%; Pred. No. 34; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FC54C5DF7B4D1B14 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Capsanthin/capsorubin synthase, chloroplast precursor.
CCS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR02086; Aldehyde_dehydr.
Pfam: PF00171; aldedh; 1.
PROSITE; PS000070; ALDEHYDE DEHYDR CYS; FALSE_NEG.
PROSITE; PS000697; ALDEHYDE DEHYDR_GLU; 1.
Oxidoreductase; NADP; Plasmid.
                                                                                                                                                                                                                                                                                                 -!- PATHWAY: 4-aminobutyrate (GABA) degradation.
                          491 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           503 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY
BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (Se or send an email to license@isb-sib.ch).
                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE000096; AAB91849.1; -. PIR; 843963; 843963.
HSSP; P05091; 1CW3.
                                                                                                                          (strain NGR234).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53253 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 62.
                                                                                                                                                                                                                                                                                     succinate + NAD(P)H.
                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   263
297
291 AA;
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                                                                                                                                                                                                   SEQUENCE FROM N.A.
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SEÇUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=2711;
                                                                                                                                                                          NCBI_TaxID=394;
                                                                                                                          Rhizobium sp.
                                                                                                            GABD OR Y4SJ.
                          GABD RHISN
P55653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITSI
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Q9SEA0;
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               GABD_RHISN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=BG1016;
Banes W.F., Kirchner M., Yoon J., Biermann C., Wang I., McCartney M.,
Verrelli B.C.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 41, Last annotation update)
Glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) (G6PD) (Fragment).
ZW OR G6PD.
-!- PATHWAY: Caroténoid biosynthesis.
-!- SUBCELLULAR LOCATION: Chloroplast; chromoplast (By similarity).
-!- SIMILARITY: BELONGS TO THE LYCOPENE CYCLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- CATALYTIC ACTIVITY: D-glucose 6-phosphate + NADP(+) = D-glucose 1,5-lactone 6-phosphate + NADPH.
-i- PATHWAY: Pentose phosphate pathway; first step.
-i- SIMILARITY: BELONGS TO THE GLUCOSE-6-PHOSPHATE DEHYDROGENASE PAMILY.
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAPSANTHIN/CAPSORUBIN SYNTHASE.
                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF169241; AAF18389.1; -.
Oxidoreductase; NAD; Carotenoid biosynthesis; Chloroplast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Length 503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2C957F0AA91075E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHLOROPLAST (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 518 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 37; DB
Pred. No. 35;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              503 AA; 56663 MW;
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HSSP; P11411; 1DPG.
FlyBase; FBgn0015691; Dyak\Zw.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila yakuba (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 64.9%;
Best Local Similarity 71.4%;
Matches 5; Conservative
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503
117
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
N. Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
M. Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Ffannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolakov S.,
Borkova D., Botchan M.R., Bouck J., Brocketein P., Brottier P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davengort L.B., Davies P.,
Cherry J.M., Cawley S., Dahlke C., Davengort L.B., Davies P.,
Cherry J.W., Doug E.E., Downes M., Dugan-Rocha S., Pleischmann W.,
Durbin K.J., Evangelista C.C., Ferriaz C., Ferriera S., Fleischmann W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=F23.3, F24.1, MT41, MT68, Z3, Z5, Z11, Z16, Z21, Z27, Z41, Z42, Z55, Z62, Z64, and Z74;
MEDLINE=97070821; PubMed=8913747;
                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eanes W.F., Kirchner M., Yoon J., Biermann C.H., Wang I.N., McCartney M.A., Verrelli B.C.; "Historical selection, amino acid polymorphism and lineage-specific divergence at the Gépd locus in Drosophila melanogaster and D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=88255872; PubMed=2838391;
Fouts D., Ganguly R., Gutierrez A.G., Lucchesi J.C., Manning J.E.;
"Nuclectide sequence of the Drosophila glucose-6-phosphate
dehydrogenase gene and comparison with the homologous human gene.";
Gene 63:261-275 (1988).
                                                                                                                                                                                                                                                                                                                                         .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                64.9%; Score 37; DB 1; Length 518; 100.0%; Pred. No. 36; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G6PD_DROME STANDARD; PRT; 524 AA.
P12646; Q27574; Q27872; Q27879; Q27881; Q3VWE2; Q9VWE3; Q1-0CT-1989 (Rel. 12, Created)
15-UUJ-1998 (Rel. 36, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
Glucose-6-phosphate 1-dehydrogenase (BC 1.1.1.49) (G6PD)
                                                                                                                                                                                                             203 203 BY SIMILARITY.
518 AA; 59938 MW; 6AFA194EID3A3E8B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
                   Pfam; PF00479; G6PD; 1.
Pfam; PF02781; G6PD C; 1.
PRINTS; PR00079; G6PDHRGNASE.
ProDom; PD001129; G6PD; 1.
TIGRENMS; TIGR00871; zwf; 1.
PROSITE; PS00069; G6P DEHYDROGENASE; 1.
Oxidoreductase; NADP; Glucose metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZW OR GGPD OR CG12529.
Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genetics 144:1027-1041(1996).
InterPro; IPR001282; GGPD.
                                                                                                                                                                                                                                                                                                         Local Similarity 100.
Les 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             506 YKWHG 510
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                 3 YKWHG 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Zwischenferment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=7227;
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                                                                                                                                                                                                             ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                 Matches
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HDD DAC DD DAC D
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RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Godek A., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J., Houston K.A., Howland T.J., Wei M.-H., Hoeyam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lang Y., Lin X., Mattei B., McIntosh T.C., McLeod M.P., Mosherson D., Markulov G., Milshian N.V., Mobarry C., Morris J., Mosherefi A., Melson D.R., Moy M., Murphy B., Murphy D., Muzny D.M., Nelson D.L., Ra Reinert K., Remington K.A., Nixon K., Nusskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Shies B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Ang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Nang X., Williams S.M., Waodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Aniliams S.M., Waodage T., Worley K.C., Wu D., Yang S., Yao Q., Zhao Gibbs R.A., Myere E.W., Rubin G.M., Venter J.C.; An H. Schong F.N., Zhong W., Zhou X., Zhu X., Zhu X., Smith H.O., The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/amnounce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Berkeley; TISSUB=Empryo; MEDLINE=22426066; PubMed=12537569; Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M., Garlson J.W., Brokstein P., Yu C., Champe M., George R.A., Guarin H., Kronmiller B., Pacleb J.M., Park S., Wan K.H., Rubin G.W., Celniker S.E.; Desource."; A Drosophila full-length cDNA resource."; Genome Biol. 3.RESEARCH0080.1-RESEARCH0080.8(2002).
-!- CATALYTIC ACTIVITY: D-glucose 6-phosphate + NADP(+) = D-glucono-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isoid=Pl2646-2; Sequence=VSP 001593;
Note=No experimental confirmation available;
SIMILARITY: BELONGS TO THE GLUCOSE-6-PHOSPHATE DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1,5-lactone 6-phosphate + NADPH.
-!- PATHWAY: Pentose phosphate pathway; first step.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=P12646-1; Sequence=Displayed;
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EMBL; M26673; AAA51463.1; JOINED.
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AAB02806.1;
AAB02807.1;
AAB02808.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=Long;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
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EMBL;
EMBL;
EMBL;
EMBL;
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AE003512; AAF48999.1;

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LSPA WIGBR
Q8D2R1;
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LSPA WIGBR
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
-!- FUNCTION: Relaxes both positive and negative superturns and
exhibits a strong decatenase activity. The B subunit binds ATP (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- CATAINTIC ACTIVITY: ATP-dependent breakage, passage and rejoining of double-stranded DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum aerophilum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Type II DNA topoisomerase VI subunit B (EC 5.99.1.3) (TopoVI-B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
R EMBL, AB003512; AAF49000.1; -.
R PIRE, A47740; AA7740.
R PIR; A47740; A47740.
A47740; A47740.
R PIR; A47740; A47740.
R PIR; A47740; A47740.
R PIR; A47740; A47740.
R PIR; A47740; A47740.
R PERM; PP00479; GFD004079; Zw.
R PERM; PP00479; GFD01.
R PERM; PP00479; GFD01.
R PERM; PR00779; GFD01.
R PERM; PR00779; GFD01.
R PERM; PR00779; GFD01.
R PERM; PR00779; GFD01.
R PRINTS; PR00069; GFD01.
R PROSTES; PS00069; GFD DEHYDROGENASE; 1.
R PR0STES; PS00069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64.9%; Score 37; DB 1; Length 524; 100.0%; Pred. No. 36; 0; Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pyrobaculum aerophilum.
Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                \label{eq:similarity} \mbox{$\text{-i-similarity}$.}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                527 A.A.
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STRAIN=IM2 / ATCC 51768 / DSM 7523;
MEDLINE=21664397; PubMed=11792869;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thermoproteaceae; Pyrobaculum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            512 YKWHG 516
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Q8ZVMO;
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                                                                              HAMAP, MF 00322, -; 1.

InterPro; IPR003594; ATPbind ATPase.

InterPro; IRR005734; DNA topEB.

Pfam; PF02518; HATPase c; 1.

SMART; SM00387; HATPase c; 1.

TIGRFAMs; TIGR01052; topEb; 1.

ISOMETASE; Topoisomerase; DNA-binding; ATP-binding; Complete proteome.

SEQUENCE 527 AA; 59870 MW; 7BAADB81F8FC9D97 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-22297718; PubMed-12219091;
Akman L., Yamashita A., Watanabe H., Oshima K., Shiba T., Hattori M.,
                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Lipoprotein signal peptidase (EC 3.4.23.36) (Prolipoprotein signal peptidase (EC 3.4.23.36)
Lipoprotein Signal peptidase (EC 3.4.23.36)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wigglesworthia glossinidia brevipalpis.
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales;
Enterobacteriaceae, Wigglesworthia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Genome sequence of the endocellular obligate symbiont of tsetse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hydrolase; Aspartyl protease; Transmembrane; Inner membrane;
                                                                                                                                                                                                                                             64.9%; Score 37; DB 1; Length 527; 100.0%; Pred. No. 36; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Probable).
-1- SIMILARITY: Belongs to peptidase family A8.
                                                                                                                                                                                                                                                                                                                                                                                                                                          153 AA.
modified and this statement is not removed.
                entities requires a license agreement (S. or send an email to license@isb-sib.ch).
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InterPro; IPR001872; SigPTase A8.
Pfam; PF01252; Peptidase A8; 1.
PRINTS; PR00781; LIPOSIGFTASE.
ProDom; PD004304; SigPTase A8; 1.
TIGRRAMS; TIGR00077; 1spA; 1.
PROSITE; PS00855; SPASE II; FALSE NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                   EMBL; AE009863; AAL64036.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AB063521; BAC24439.1; -.
                                                                                                                                                                                                                                                             Local Similarity 100.
1es 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                 162 YKWHG 166
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                                                                                                                                                                                                                                                                                                                3 YKWHG 7
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STRAIS-ATC 15692 / PAO1;
STRAIS-ATC 15692 / PAO1;
SCORTING-ATC 15692 / PAO1;
SCORTING-ATC 15692 / PAO1;
SCORTING-ATC 15692 / PAO1;
SCORTING-ATC 15692 / PAO1;
HICKEY M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAINS-ATCC 15692 / PAO1;
MEDLINE-ATCC 15692 / PAO1;
MEDLINE-92269572; PubMed-1588814;
MEDLINE, Filloux A., Akrim M., Ball G., Lazdunski A., Tommassen J.;
Bally M., Filloux A., Akrim M., Ball G., Lazdunski A., Tommassen J.;
"Protein secretion in Pseudomonas aeruginosa: characterization of
seven xcp genes and processing of secretory apparatus components by
prepilin peptidase.";
Mol. Microbiol. 6:1121-1131(1992).
                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 406:959-964(2000).

-:- FUNCTION: INVOLVED IN A GENERAL SECRETION PATHWAY (GSP) FOR THE EXPORT OF PROTEINS. REQUIRED FOR THE TRANSLOCATION OF A VARIETY OF ENZYMES ACROSS THE OUTER MEMBRANE.

-:- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales,
Pseudomonadaceae, Pseudomonas.
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                                                                                                                                                                                                        63.2%; Score 36; DB 1; Length 153; 66.7%; Pred. No. 17; 1. 2; Mismatches 0; Indels
                                                                                     Potential.
BY SIMILARITY.
BY SIMILARITY.
1AEE3B201E935B58 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DBC-1992 (Rel. 24, Created)
01-DBC-1992 (Rel. 24, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         405 AA.
                                        Potential.
Potential.
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Interpro; IPR001992; Bact secr systII.
                 Potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       General secretion pathway protein F. XCPS OR PA3102.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
               7 24 POI
60 79 POI
86 108 POI
123 145 POI
105 105 BY
132 132 BY
153 AA; 18085 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AE004734; AAG06490.1; -.
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                                                                                                                                                                                                                                                           4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  opportunistic pathogen."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; S25385; SKPSXS.
                                                                                                                                                                                                                                                                                                                                                119 YIYKWH 124
                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                          1 FLYKWH 6
Complete proteome
TRANSMEM 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=287;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             GSPP_PSEAE

AC G00513,
DT G00513,
DT 01-DEC-1992
DT 01-DEC-1992
DT 16-OCT-2001
DE General secre
GN XCRS OR PA31GOS
OC Bacteria; Pro
OC STRAIN=9226
RX MEDLINE=9226
RX MEDLINE=9243;
RX MEDLINE=2043;
CC RX MEDLINE=2043;
CC PROSEDLUIC
CC PROSEDLUIC
CC PROBEDLUIC
CC PROSEDLUIC
CC PROBEDLUIC
CC CO SIMILARI;
CC C This SMISS-PR
CC C This SMISS-PR
CC C SEMBL; AEO0447;
DR PIRE, 253385;
DR INTER-PRO; IRP
                                        TRANSMEM
TRANSMEM
TRANSMEM
ACT SITE
ACT SITE
ACT SITE
                                                                                                                                                                                                                Query Match
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from Xanthomonas oryzae pv. oryzae.";
Mol. Gen. Genet. 244:383-390(1994).
-!- FUNCTION: THIS METHYLASE RECOGNIZES THE DOUBLE-STRANDED SEQUENCE CRATCG, CAUSES SPECIFIC METHYLATION ON C-? ON BOTH STRANDS AND PROTECTS THE DNA FROM CLEAPAGE BY THE XORII ENDONUCLEASE.
-!- CATALYTIC ACTIVITY: 9-adenosyl-L-methionine + DNA cytosine = S-adenosyl-L-homocysteine + DNA 5-methylcycosine.
-!- SIMILARITY: BELONGS TO THE C5-METHYLTRANSFERASE FAMILY.
                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xanthomonas oryzae (pv. oryzae).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
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01-0CT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Modification methylase XorII (EC 2.1.1.73) (Cytosine-specific methyltransferase XorII) (M.XorII).
Pfam, PF00482; GSPII_F: 1.
PRINTS; PR00812; BCTERIALGSPF.
PROSITE; PS00814; T25P F: 1.
Transport; Transmembraïe; Inner membrane; Complete proteome.
                                                                                                                                                       63.2%; Score 36; DB 1; Length 405; 55.6%; Pred. No. 42; tive 2; Mismatches 2; Indels
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HSSP, P20869; 1DCT.
REBASE; 3534; M.XorII.
InterPro; 1PR001525; C5 DNA meth.
PRINTS, PR00105; C5METTRRRASE.
TIGRNOAF; P3 MTARE 1; 1.
PROSITE; P300094; C5 MTASE 1; 1.
PROSITE; P300095; C5 MTASE 1; 1.
PROSITE; P300095; C5 MTASE 2; 1.
Transferase; Methyltransferase; Restriction system.
ACT SITE
83 83 89 89 81 MLARITY.
SEQUENCE 424 AA; 46971 MW; F2EEB12F09918781 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F2EEB12F09918781 CRC64;
                                                                                                                      405 AA; 44061 MW; BEE59B58724C167E CRC64;
                                                                                                                                                                                                                                                                                                                                                  424 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Pred. No. 44; iive 0; Mismatches
                                                                     POTENTIAL.
                                                                                       POTENTIAL.
                                                                                                        POTENTIAL
                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=JW89011;
MEDLINE=94359461; PubMed=8078464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U06424; AAA50432.1; -.
                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                     189
239
397
                                                                                                                                                                                                                                                            248 FRERWHGFL 256
                                                                                                                                                                                                                             1 FLYKWHGFV 9
                                                                                                                                                                        Local Similarity
es 5; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=64187;
                                                                       169
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Search completed: December 16, 2003, 14:15:13
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                                                                                                                                                                                                                                                                                         Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J., Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S., Qian Y., Li S., Zhu H., Najar F., Lai H., White J., Roe B.A., Ferretti J.J., "Genome sequence of Streptococcus mutans UA159, a cariogenic dental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00987; TRNAŠYNTHGĽU.
TIGRRAMS; TIGR00464; gltx, bact; 1.
PROSITE; PS00178; AA TRNA, Lack; 1; 1.
Aminoacyl-tRNA synthētase; Proteïn biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439 (2002).

-!- CATALYTIC ACTIVITY: ATP + L-glutamate + tRNA(Glu) = AMP + diphosphate + L-glutamyl-tRNA(Glu).

-!- SUBJUNIT: Monomer (By similarity).

-!- SUBCELLULAR LOCATION: Cytoplasmic.

-!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                              15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Glutamyl-tRNA synthetase (EC 6.1.1.17) (Glutamate--tRNA ligase)
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                                                                                                                                                                                         Streptococcus mutans.
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
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258 258 ATP (BY SIMILARITY).
485 AA; 55720 MW; DFALE99DOCD1363F CRC64;
                                                                                       485 AA
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                                                                                                                                                                                                                                                                  ATCC 700610 / Serotype C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAWAR, MF 00022; -; 1.
InterPro; IPR004527; GltX bact.
InterPro; IPR00924; Glu tRNA-synt_lc.
InterPro; IPR001412; tRNA-synt_l.
                                                                                                                                                                                                                                                                               MEDLINE=22295063; PubMed=12397186
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                                                                                       STANDARD;
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                         337 KWHGF 341
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es 5; Conserv
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
KWHGF 8
                                                                                                                                                                                                                           NCBI_TaxID=1309;
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                                                                                       STRMU
 4
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SYE STRMU
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Matches
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486 AA.

PRT;

 SYE STRPN
 STANDARD;
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 ID SYE STRPN
 STANDARD;
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 AC Q97NG1;
 DT 15-SEP-2003 (Rel. 42, Created)

RESULT 15

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                                                                                                                                                                                                                                                                                                                                                                             STRAIN=ATCC BAA-334 / TIGR4;
MEDLINE=2135-209; PubMed=11463916;
Tettelin H., Nelson R.E., Paulsen I.T., Eisen J.A., Read T.D.,
Tettelin H., Nelson R.E., Paulsen I.T., Eisen J.A., Read T.D.,
Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,
McDonald L.A., Peldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
"Complete genome sequence of a virulent isolate of Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HAMAP, MF 0002; -; 1.

InterPro; TPR004527; GltX bact.

InterPro; IPR004527; GltX bact.

InterPro; IPR001412; tRNA-synt_Ic.

PFam; PF00749; tRNA-synt_Ic; 1.

PRINTS; PR00987; TRNA-SYNTHGLU.

IGREMA; TGR00464; GltX bact; 1.

PROSITE; PS00178; AA TRNA_LGASE I; 1.

Aminoacyl-RNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pneumoniae.";
Science 293:498-506(2001).
-!- CATALYTIC ACTIVITY: ATP + L-glutamate + tRNA(Glu) = AMP +
diphosphate + L-glutamyl-tRNA(Glu).
-!- SUBUNIT: Monomer (By similarity).
-!- SUBUNIT: Monomer (Cytoplasmic.
-!- SUBCELIULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Glutamyl-tRNA synthetase (EC 6.1.1.17) (Glutamate--tRNA ligase)
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                                                                                                                                                                           Streptococcus pneumoniae.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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ATP (BY SIMILARITY)
72EF5FDF704B3011 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
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PIR; C95242; C95242.
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December 16, 2003, 14:09:45; Search time 25 Seconds (without alignments) 92.899 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Q27598 drosophila	Q9v896 drosophila	Q9y0b3 sarcophaga	044249 manduca sex	Q9aw53 guillardia	Q8xi15 clostridium	Q8ilp5 plasmodium	Q95r43 drosophila	Q9w1v6 drosophila	Q8ilf6 drosophila	Q9blg6 bombyx mori	Q9gu90 bombyx mori		076208 hyphantria	Q8r946 thermoanaer	Q8i8d7 entamoeba h
SUMMARIES	αI	Q27598	968060	Q9Y0B3	044249	Q9AW53	. Q8X115	OSILPS	Q95R43	Q9W1V6	QBI1F6	O9BLG6	Q9GU90	027452	076208	5 Q8R946	Q818D7
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Q9Eqz5 bacillus ps Q8Elv6 oceanobacil Q9wu06 rattus norv Q8zdt O yersinia pe Q9Tuy7 sulfolobus Q91ja6 arabidopsis Q91ja6 arabidopsis Q91ja6 arabidopsis Q91g4 sarcophaga P70811 bacillus ha Q8404 vibrio vuln Q1250 saccharomyc Q7251 beet soil-b Q95jt8 macaca fasc Q8wyil homo sapien Q95jt8 macaca fasc Q8wyil homo sapien Q95jt8 misteria in Q8y698 listeria in Q8y698 pimpla hypo Q8cmw9 staphylococ Q8cmw9 staphylococ Q8cmy9 pasteurella Q9ctr2 mus musculu Q99n31 mus musculu	RESULT 1 Q27598 10 CONVOL-1996 (TERBELEG) 01, Created DEC DT 01-NOV-1996 (TERBELEG) 12, Lafe annotation update) 10 TO 01-NOV-1996 (TERBELEG) 12, Lafe annotation update) 10 CONVOL-1996 (TERBELEG) 12, Lafe annotation update) 11 CONVOL-1996 (TERBELEG) 12, Lafe annotation update) 12 CONVOLED 12 CONVOLED 12, Lafe annotation update) 13 CONVOLED 12 CONVOLED 12, Lafe annotation update) 14 CONVOLED 12 CONVOLED 12, Lafe and Lafe 20 CONVOLED 12, LAFE 20
Q9RGZ5 Q8ELV6 Q9WU06 Q9WU06 Q9LJA6 Q9LJA6 Q9LJA6 Q9Y0B4 P70811 Q8Y0B4 Q12350 Q72591 Q9X11 Q9X21	PRT; Created; Lager sequent and lates lates and lates a
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adamstides P.G., Scherer S.E., Lis P.W., Hoskins R.A., Galle R.F.,

George R.A., Lewis S.E., Richards S., Champen M., Feiffer B.D.,

RA Brandon R.C., Rogers Y.H.C., Blazed R.G., Champen M., Feiffer B.D.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basua A., Baxendale J., Bayraktarogulu L., Basaley E.M.,

RA Beson K.Y., Benos P.V., Bernan B.P., Bhaddari D., Bolshakov S.,

RA Beson K.Y., Benos P.V., Bernan B.P., Bhaddari D., Bolshakov S.,

RA Berkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cavaley S., Dahlke C., Davenport L.B., Davies P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cavaley S., Dahlke C., Davenport L.B., Davies P.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Grobs A., Gonrell J.H., Gu Z., Guan P., Harris M.,

RA Glodek A., Gonrell J.H., Gu Z., Guan P., Harris M.,

RA Glodek A., Gonrell J.H., Howland T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Alazlon M., Mathorsh Y.C., McLood M.P., Moshrefi A.,

Alux, Mattei B., McIntosh T.C., McLood M.P., Moshrefi A.,

RA Liux, Mattei B., McIntosh T.C., McLood M.P., Parin V., Reese M.G.,

RA Alazzolo M., Fittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Shire B.C., Siden-Kianders R., Nather B., Wang X.,

RA Shire B.C., Siden-Kiand D.A., Weinstenbach J.,

RA Shires R., Tector C. Turner R., Wentler E., Wang X.,

Rang Z.-Y., Wassarman D.A., Weinstock G.M., Wang X., Wallsham S.M., Wooldege T., Worley C.C., Wu D., Yang S., Yao Q.A.,
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Meptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                         5; Length 690;
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605 L -> V (IN STRAIN BERKELEY).
79090 MW; 7F2D6564651B1F58 CRC64;
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Last annotation update)
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Pred. No. 36;
2; Mismatches
                   Ffan; PF00372; hemocyanin; 1.
Pfan; PF0372; hemocyanin C; 1.
Pfan; PF0372; hemocyanin N; 1.
PRINTS; PR00187; HAEMOCYANIN.
PROSITE; PS00209; HEMOCYANIN.;
PROSITE; PS00210; HEMOCYANIN.; 1.
PROSITE; PS00498; TYROSINASE Z; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
InterPro; IPR002227; Tyrosinase.
                                                                                                                                                                                                                  Oxidoreductase; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                    75.48;
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01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2002 (TrEMBLrel. 22,
BC Gene product (GH04080P).
BC OR CG5779.
                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 71.5
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 404 YRWHGFI 410
                                                                                                                                                                                                                                                                                                    690 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                        VARIANT
                                                                                                                                                                                                                                            VARIANT
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Prerygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Oestroidea,
Sarcophagidae, Sarcophaga.
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Glibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                              STRAIN=Berkeley;
Staptecon M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise B., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
Munco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AROO3801; AARS7775.1;
EMBL, AROS03801; AARS7775.1;
EMBL, PASSP; PO4253; ILLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
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Pred. No. 36;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

MEDLINE=20359206; PubMed=10899462;
Chase M.R., Raina K., Bruno J., Sugumaran M.;

Furification; characterization and molecular cloning of prophenoloxidaes from Sarcophaga bullata.,;

Insect Blochem. Mol. Biol. 30:953-967(2000).

EMBL; AF161261; AAD45527.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF0372; hemocyain; 1.
Pfam; PF0372; hemocyanin_C; 1.
Pfam; PF0372; hemocyanin_C; 1.
PRINTS; PF03123; hemocyanin_N; 1.
PROSTIE; PF030209; HEMOCYANIN_1; 1.
PROSTIE; PF00210; HEMOCYANIN_1; 1.
PROSTIE; PF00210; HEMOCYANIN_2; 1.
PROSTIE; PF00498; TYROSINASE 2; 1.
SEQUENCE 690 AA; 79090 MW; 49FC131F12D0B893 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          691 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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InterPro; IPR001896; Hemccyanin.
InterPro; IPR005203; hemccyanin. C.
InterPro; IPR005204; hemccyanin.N.
InterPro; IPR002277; Tyrosinase.
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InterPro; IPR05203; hemocyanin C.
InterPro; IPR005204; hemocyanin T.
InterPro; IPR00504; hemocyanin N.
InterPro; IPR00527; Tyrosinase.
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Pfam; PF0372; hemcoyanin_C; 1.
Pfam; PF0372; hemcoyanin_N; 1.
PRINTS; PR00187; HARNCYANIN_1: PROSITE; PS00209; HEMCCYANIN_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75.4%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 71.4
nes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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404 YRWHGFI 410
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                                                                                                                            SEQUENCE FROM N.A.
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Matches
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Query Match
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Ubiquitin-conjugating enzyme E2-21 KD (EC 6.3.2.19) (Ubiquitin-protein UCE-E2.
                                                                                                                                                                                                                                                                                                                                                044249;
01-UN-1998 (TrEMBLrel. 06, Last sequence update)
01-UN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Pro-phenol oxidase subunit 1 (EC 1.14.18.1).
Manduca sexta (Tobacco hawmeth) (Tobacco hornworm).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingiodea;
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                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENGUENCE FROM N.A.

MEDLINE-98135121; PubMed-9474780;

A.Ulang H., Wang Y., Ma C., Kanost M.R.;

Subunit composition of pro-phenol oxidase from Manduca sexta:

"Subunit composition of pro-phenol oxidase from Manduca sexta:

Insect Blochem. Mol. Biol. 27:835-850(1997).

EMBL; ARO0325; AAC05796.1; -.

EMBL; ARO0325; AAC05796.1; -.

R HSSP; P04253; 10XY.

R InterPro; IPR005203; hemocyanin.

R InterPro; IPR005203; hemocyanin.

R InterPro; IPR005204; Tyrosinase.

R Pfam; PF03722; hemocyanin. C; 1.

R Pfam; PF03722; hemocyanin. C; 1.

R Pfam; PF03722; hemocyanin. C; 1.
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                                                                                             75.4%; Score 43; DB 5; Length 691; 71.4%; Pred. No. 36; tive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
               PROSITE; PS00030; RRW RNP 1; 1.
PROSITE; PS00498; TYRŌSINĀSE 2; 1.
SEQUENCE 691 AA; 79796 MW; DD7545E82CABC94D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          685 AA; 78965 MW; BE5811D145302583 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Guillardia theta (Cryptomonas phi).
Eukaryota, Cryptophyta, Cryptomonadaceae; Guillardia.
NCBI_TaxID=55529;
                                                                                                                                                                                                                                                                                                                              685 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
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PROSITE; PS00209; HEMOCYANIN 1; 1.
PROSITE; PS00210; HEMOCYANIN 2; 1.
PROSITE; PS00498; TYROSINASE 2; 1.
Oxidoreductase.
                                                                                                                                                                                                                                                                                                                              PRT;
  PROSITE; PS00210; HEMOCYANIN 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sphingidae; Sphinginae; Manduca.
                                                                                Ouery Match
Best Local Similarity 66...
6; Conservative
                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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404 YRWHGFI 410
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044249

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DT 01-40

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MEDLINE=2122349; PubMed=11323671;
MEDLINE=21223349; PubMed=11323671;
MEDLINE=21223349; PubMed=11323671;
MEDLINE=21223349; PubMed=11323671;
MEDLINE=21223349; PubMed=11323671;
MEDLINE 4:0:1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-1.091-
                                                                      Zauner S., Fraunholz M., Wastl J., Penny S.L., Beaton M., Cavalier-Smith T., Maier U., Douglas S.; "Chloroplast protein and centrosomal genes, a tRNA intron, and odd telomeres in an unusually compact eukaryotic genome, the cryptomonad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium.
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PROSITE; PS50127; UBIQUITIN_CONJUGAT_2; 1.
Ligame; Ubl conjugation pathway.
SEQUENCE 144 AA; 16365 WW; D8D4B2DD6EF74E80 CRC64;
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Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002)
BMBL; AP003193; BAB82015.1;
Interpro; IFR001360; Glyco.hydro.1.
Pfan; PP00223; Glyco.hydro.1; 1.
PRINTS; PR00131; GLHYDRLASE1.
ProDom; PD000650; Glyco.hydro.1; 1.
                                                                                                                                                                                                                                                                           nucleomorph.";
Proc. Natl. Acad. Sci. U.S.A. 97:200-205(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
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InterPro; IPR000608; UBQ_conjugat.
Pfam; PF00179; UQ_con; 1.
ProDom; PD000461; UBQ_conjugat; 1.
SMART; SM00212; UBCc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
SEQUENCE FROM N.A.
MEDLINE=20087226; PubMed=10618395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clostridium perfringens.
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Matches 6, Conserva
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PubMed=11792842;
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Beta-glucosidase.
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Query Match
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Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
Carlton J.M., Nelson K.E., Bowman S., Paulsen I.T., James K.,
Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
Chan M.-S., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S.,
Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Weoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF14_0199.
Plasmodium falciparum (isolate 3D7).
Bukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
                        71.9%; Score 41; DB 16; Length 459; 100.0%; Pred. No. 52; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1149;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 41; DB 5; Length 113
Pred. No. 1.38+02;
2; Indels
                                                                            Indels
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Hypothetical protein.
SEQUENCE 1149 AA; 137812 MW; 5C3B42A34DCCBFCD CRC64;
                                                                                                                                                                                                                                                                                                                                                        01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Last annotation update)
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66.7%;
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01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2003 (TrEMBLrel. 23,
Query Match
Best Local Similarity luv...
                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
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les 6; Conserv
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Q8ILP5;
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REDINESERREIEY,
RX MEDINESERREIEY,
RX Adams N.A.
REDINESERREIEY,
RA Adams N.D., Cellniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adamstides P.G., Scherer S.E., Li P.W., Hoskins R.A., Calle R.F.,
RA Adamstides P.G., Scherer S.E., Li P.W., Hoskins R.A., Calle R.F.,
RA Adamstides P.G., Scherer S.E., Li P.W., Hoskins R.A., Calle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Ffeiffer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Rasley E.M.,
RA Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basun A., Baxendla B.P., Bhandari D., Bolahkov S.,
RA Borkova D., Bocchan M.R., Bouck J., Barnan B.P., Bhandari D., Bolahkov S.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Pavenport L.B., Davies P.,
RA Posler C., Gabriellan A.E., Garra C., Ferriar S., Ferischmann W.,
RA Posler C., Gabriellan A.E., Garra C., Ferriar S., Ferischmann M.,
RA Hortin D., Houston K.A., Howland T.J., Hernandez J.S., Hurris M.,
Harris N.L., Harvey D., Helman T.J., Hernandez J.S., Moshrefi A.,
Hostin D., Houston K.A., Howland T.J., Mernison J.A., Lin X.,
RA Hostin D., Houston K.A., Howland T.J., Mernison D.M., Nalson D.L.,
RA Harris N.L., Marvey D., Murphy E., Smith T.,
RA Reinert K., Remington K., Supskin M., Stupski M. P., Smith T.,
RA Reinert K., Remington K., Stupski M. P., Smith T.,
RA Bine B.C., Siden-Kiamos I., Simpson M., Skupski M. P., Smith T.,
Ry Spier E., Spradling A.C., Stapleton M., Strong R., Svirskas R., Tector C., Turner R., Wentesse R.,
Ry Spier S., Spradling A.C., Stapleton M., Strong R., Svirskas R., Fercer C., Turner R., Wentesse R.,
Ry Spier S., Spradling A.C., Stapleton E., Spradling A.C., Stapleton M., Strong R., Stap
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                               Score 40; DB 5; Length 683;
Pred. No. 1.1e+02;
1; Mismatches 1; Indels
InterPro, IRR000896; Hemocyanin.
InterPro, IRR005203; hemocyanin.C.
InterPro, IRR005203; hemocyanin.N.
InterPro, IRR005227; Tyrosinase.
Pfam; PF00372; hemocyanin, 1.
Pfam; PF00372; hemocyanin, 2; 1.
Pfam; PF00372; hemocyanin, N.
PR0517E; PS00209; HEMOCYANIN N.
PROSITE; PS00209; HEMOCYANIN N.
PROSITE; PS00210; HEMOCYANIN N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9W1V6;
01-WAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           683 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 71.4%;
5; Conservative
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403 YKWHAFI 409
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DOX-A3 OR CG2952.
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Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
Zhong X.H., Zhong W., Zhou X., Zhu X., Smith H.O.,
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

The genome sequence of Drosophila melanogaster.";
Science 297:2185-2195(2000).

EMBL: AEG01459; AAF46946.1; -.

RISSP: PO4253; IOXY.

RISSP: PO4253; IOXY.

RISSP: PO4253; IOXY.

RISSP: PO4253; IOXY.

RICEPTO; IPRO05203; Hemocyanin.

RICEPTO; IPRO05204; hemocyanin.

RICEPTO; REMOCYANIN.

REMITS; PRO0187; HAEMCCYANIN.

REMOSITE; PS00209; HEMOCYANIN.

REMOSITE; PS00209; HEMOCYANIN.

REMOSITE; PS00409; TYROSINASE Z.;

SEQUENCE 683 AA; 79314 MM; 437CBDD9E8A278BF CRC64;
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STRAIN=Tucson 14021-0224.0;
MEDLINE=22426072; PubMed=12537575;
Bergman C.M., Pfeiffer B.D., Rincon-Limas D.E., Hoskins R.A.,
Gnirke A., Mungall C.G., Wang A.M., Krommiller B., Pacleb J., Park S.,
Stapleton M., Wan K., George R.A., de Jong P.J., Botas J., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Bukaryota, Metazoa, Arthropoda; Hexapoda; Insecta, Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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01-JUN-2001 (TrEMBLrel. 17, Created)
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Best Local Similarity 71.4
Matches 5; Conservative
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Best Local Similarity
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0811F6
1D 01-MAD
DT 01-MAD
DT 01-MAD
DD 00x-A,
DD 00x-A,
DC 00x Dxoso
OC Dxoso
OC Dxoso
OX NCBI-
RR SEQUES
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EMBL, AF179461, AAG09303.1; -.

INTERFY: P04553; 10XY.

INTERFY: P179461, PR006869; Hemocyanin.

InterPro; IPR0062209; hemocyanin. C.

InterPro; IPR0052209; hemocyanin. N.

InterPro; IPR0052209; hyposinase.
                                                                            Bukaryota: Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
Bombycidae; Bombyx.
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Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
Bombycidae; Bombyx.
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                                                                                                                                                                                                                                                     MEDLINE=21179161; PubMed=11118441;
MEDLINE=21179161; PubMed=11118441;
MEDLINE=21179161; PubMed=11118441;
MEDLINE=21179161; PubMed=11118441;
MCULICULAR Pro-phenoloxidase of the silkworm, Bombyx mori.
Purification and demonstration of its transport from hemolymph.";
Purification and demonstration of its transport from hemolymph.";
EMBL; AB048761; BAB40959.1; --
HSSP; P04253; LOXY.
InterPro; IPR006204; Hemocyanin.
InterPro; IPR005204; Hemocyanin.
InterPro; IPR005204; Tyrosinase.
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Ishiguro M.;
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1-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Prophenoloxidase-2 (EC 1.14.18.1).
01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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PROSITE, PS00210; HEMOCYANIN_2; 1.
PROSITE; PS00498; TYROSINASE, 2; 1.
SEQUENCE 693 AA, 80181 MW.
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PROSITE; PS00210; HEMOCYANIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00372; hemocyanin; 1.
Pfam; PF03723; hemocyanin, C; 1.
Pfam; PF03722; hemocyanin, N; 1.
PRINTS; PR00187; HAEMOCYANIN.
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Pfam; PF03723; hemocyanin C; 1.
Pfam; PF03722; hemocyanin N; 1.
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Best Local Similarity 44...
4; Conservative
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                           01-MAR-2003 (TrEMBLrel. : Prophenoloxidase-2s. Bombyx mori (Silk moth).
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SEQUENCE 268 AA
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Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
Bombycidae; Bombyx.
                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=KINSHU X SHOWA; TISSUE-Hemocyte;
MEDLINE=95372362; PubMed=7644494;
Kawabata T., Yasuhara Y., Ochiai M., Matsuura S., Ashida M.;
"Molecular cloning of insect pro-phenol oxidase: a copper-containing protein homologous to arthropod hemocyanin.";
Proc. Natl. Acad. Sci. U.S.A. 92:7774-7778(1995).
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01-07AN-1999 (TrEMBLrel. 09, Last sequence update)
01-MR-2003 (TrEMBLrel. 23, Last annotation update)
PROPHENOLOXIDASE subunit 2 (EC 1.14.18.1) (PROPHENOLOXIDASE-2F).
Bombyx mori (Silk moth).
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"Pro-phenoloxidase type-2(f) 2.3 kbp Bombyx mori.";

Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AB04937L; BAR08369.1; -.

EMBL; AB049762; BAB41101.1; -.

EMBL; AB049762; BAB41101.1; -.

EMBL; AB04253; LOXY.

InterPro; IPR002203; hemocyanin. C.

InterPro; IPR002203; hemocyanin. N.

InterPro; IPR002203; hemocyanin. N.

InterPro; IPR002204; Tyrosinase.

Pfam; PF03722; hemocyanin. C:

Pfam; PF03722; hemocyanin. N. 1.
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                                                                                                                      Match 70.2%; Score 40; DB 5; Length 693; Local Similarity 44.4%; Pred. No. 1.1e+02; tes 4; Conservative 3; Mismatches 2; Indels
                                  Oxidoreductase.
SEQUENCE 693 AA; 79994 MW; FD71A7593A9312EB CRC64;
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PROSTIE: PS00209; HEMOCYANIN 1; 1.
PROSITE; PS0010; HEMOCYANIN 2; 1.
PROSITE; PS00499; TYROSINASE_2; 1.
PROSITE; PS00498; TYROSINASE_2; 1.
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SEQUENCE 693
                                                                                                                                Query Match
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December 16, 2003, 14:06:05; Search time 33 Seconds (without alignments) 43.289 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	Human cancer antiq	C qlutamicum prote	Human cancer antiq	Human cancer antiq	Drosophila melanog	Human protein SEO	Human prostate can	Human ORFX protein	N-terminal fragmen
SUMMARIES			ID	AAU74682	**************************************	AAU74685 ·	AAU74684	ABB63728	ABP64908	AAB56395	ABP00720	AAR57000
			В	23	22	23	23	22	23	21	23	15
			e Match Length DB 1	1 0	1043	σ	6	979	1044	102	79	25
	æ	Query	Match]	100.0	82.7	78.8	76.9	75.0	75.0	73.1	71.2	69.2
			Score	52	43	41	40	39	39	38	37	36
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	e 2	ın u	67.3	15	23	AA026506	Huma	Human topoisomeras
	35	o ro	67.3	53	22	AAM83305	Huma	cobactel pylor n immune/haema
, .	9.0	ro r	67.3	72	53	ABU51593	Heli	cobacter pylor
7 (*)	38	υw	67.3	84	23 2	ABU52086 ABU51112	Heli	cobacter pylor cobacter pylor
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- 4	9 -	n r	67.3	80 80 44 17	23	ABU51780 AA026505	Himan	bacter fonoise
٠,٠	2 2	ı m	67.3	88	23	ABU51873	Heli	bacter
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4	. 2	ı w	67.3	163	23	ABU50727	1 ·H	cobacte
						ALIGNMENTS		
RESULT 1	T 1							
8	AAU74682		standard;	l; Peptide	ide;	9 AA.		
{ & }	AAU74682	82;						
15	09-APR	-2002	(fir	rst entry	رکز			
(日)	Human	cancer	antigen		ATF4/CREB-2	based	immunogenic ligand #	2.
(222)	Human; immunog adopti	cancer genic l	r ant ligan unoth	Human; cancer antigen; Alimmunogenic ligand; gene adoptive immunotherapy;	TF4; C thera cancer	REB-2; vac py; MHC, m ; overian	cine, cytostatic, major histocompatibil cancer.	lity complex;
808	Homo sapie Synthetic	apiens tic.				\		
X & S	WO200192306		-A2.		\			
12;	06-DEC	-2001.		<u>'</u> '	ι			
5 E S	30-MAY	-2001;		2001WO-US17454	7454.			
8 E E E	31-MAY-2	-2000;	2000US-	US-209388P. US-257007P.	188P.	,		
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The invention relates to compounds comprising an immunogenic ligand whose sequence is based in part on residues 42-50 of human cancer antiglem AFF4/CRBE-2 foot defined) and the polynucleotides encoding them. Also included are an antibody that specifically recognises and binds the compound, a method for inducing an immune response in a subject by delivering the compound, a method of immunotherapy comprising the compound, a method of immunotherapy comprising administering to a subject the antibody, an immuno effector cell that has been raised in vitro or in vivo in the presence and at the expense of an antibod presenting coll that presents the immunogenic compound in the context of an MHC (major histocompatibility complex) molecule and a method of adoptive immunotherapy comprising administering the immune especially useful in gene therapy or as compounds. The compounds are useful for reating an immune response to the synthetic and naturally occurring compounds. The compounds are useful for reating cancer, particularly covarian cancer. The compounds are useful for reating anniant stream to ancier. The compounds are useful for reating annibodies are further useful for immunotherapy when administered to a subject. The peptides, polypeptides and polymuclectides are useful in diagnostic methods, for the detection and purification of antibodies, or as immunogens for the production of antibodies. The present sequence represents a human cancer and antibodies. The present sequence represents a human cancer and antibodies.
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New therapeutic compounds comprising immunogenic ligands, useful for
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                      modulating an immune response, particularly for treating ovarian cancer, and as components of anticancer vaccines
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 52; DB 23; 100.0%; Pred. No. 9.3e+05; vative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C glutamicum protein fragment SEQ ID NO: 6647.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAG92893 standard; Protein; 1043 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              degeneracy of the DNA sequences.
                                                                                   Claim 2; Page 55; 68pp; English.
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07-APR-2000; 2000JP-0159162.
03-AUG-2000; 2000JP-0280988.
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Best Local Similarity
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The present invention provides a number of nucleotide and protein agequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacterium, coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Soryneform bacterium, and identifying a monoganic acids, particularly L-lysine. The present seacharides and organic acids, in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; cancer antigen; ATF4; CREB-2; vaccine; cytostatic; immunogenic ligand; gene therapy; MHC; major histocompatibility complex; adoptive immunotherapy; cancer; ovarian cancer.
                                                                                                                                                                                                                                                                                                                                                                                                     Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                  Novel polymucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
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                                                                                                                                                                                 Claim 17; SEQ ID NO: 6647; 246pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82.7%; Score 43; DB 22; Length 1043; 77.8%; Pred. No. 27; cive 0; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human cancer antigen ATF4/CREB-2 based immunogenic ligand #5.
Tateishi N, Senoh A, Ikeda M, Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU74685 standard; Peptide; 9 AA.
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20-DEC-2000; 2000US-257007P.
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                                     WPI; 2001-376931/40.
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                                                       N-PSDB; AAH68112
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The invention relates to compounds comprising an immunogenic ligand whose sequence is based in part on residues 42-50 of human cancer antispen Arra/CREB-2 (not defined) and the polynuclecides encoding them. Also included are an antibody that specifically recognises and binds the compound, a method for inducing an immune response in a subject by delivering the compound, a method of immunotherapy comprising the subject the antibody. An immune effector cell that has central presenting cell that presents the immunogenic compound in the context of an MHC (major histocompatibility complex) molecule and a context of an MHC (major histocompatibility complex) molecule and a ceffector cell. The compounds are useful for modulating an immune response to the synthetic and naturally occurring compounds. The compounds are useful for treating cancer, particularly cacines. The compounds are useful for treating cancer, particularly covariant cancer. The compounds are also useful for generating antibodies that specifically recognise and bind to these molecules. These antibodies are further useful for immunotherapy when administered to a subject. The peptides, polypeptides and polynuclecides are useful in classification of antibodies. The peptides, polypeptides and polynuclecides are useful in classification of antibodies. The percent in the production of antibodies. The present incomponents of the production of antibodies. The present immunogenic methods in the production of antibodies. The present immunogenic matuser antigen ATF4/CREB-2 based immunogenic
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Claim 5; Page 56; 68pp; English.
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20-DEC-2000; 2000US-257007P.
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Matches 7; Conservative
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The invention relates to compounds comprising an immunogenic ligand whose sequence is based in part on residues 42-50 of human cancer antigen ATE4/CREB-2 (not defined) and the polymuclectides encoding them. Also included are an antibody that specifically recognises and binds the compound, a method for inducing an immune response in a subject by delivering the compound, an enthod of immunotherapy comprising administering to a subject the antibody, an immune effector cell that has been raised in vitro or in vivo in the presence and at the expense of an antibog presenting cell that presents the immunogenic compound in the context of an MHZ (major histocompatibility complex) molecule and a method of adoptive immunotherapy comprising administering the immune response to the synthetic and naturally occurring compounds are sepecially useful in gene therapy or as compounds. The compounds are specially useful in gene therapy or as compounds of anti-cancer vaccines. The compounds are useful for treating cancer, particularly covarian cancer. The compounds are useful for these molecules. These that specifically recognise and bind to these molecules. These cancer the compounds are larged the information of administered to a minimal cancer was an effected to a manner was an effected 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           subject. The peptides, polypeptides and polynucleotides are useful in diagnostic methods, for the detection and purification of antibodies, or as immunogens for the production of antibodies. The present
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New therapeutic compounds comprising immunogenic ligands, useful for
                            for treating ovarian
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                          modulating an immune response, particularly for t cancer, and as components of anticancer vaccines
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                                                                                                             Claim 4; Page 56; 68pp; English.
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11-JUL-2000; 2000US-0614150.
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB63728
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Human; expressed sequence tag; BST; hemanopoietic disorder; central nervous system disease; viral infection; peripheral nervous system disease; non-healing wound; infection disorder; bacterial infection; allergy; cancer; fungal infection; autoimmune disorder; bacterial infection; allergy; cancer; antiallargic, autointy; immunosuppressive; neuroprotective; oytostatic; haemostatic; virucide; autibacterial; fungicide;
                                                                                                                                                                       capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                             The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                  New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tang YT, Goodrich RW, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA;
Ren F, Xue AJ, Yang Y, Wehrman T, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated polynucleotide, useful in research, diagnostic or therapeutic methods, e.g. preventing or treating disorders involving aberrant protein expression or biological activity
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                        The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                          insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                       Disclosure; SEQ ID NO 17976; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                   75.0%; Score 39; DB 22; Length 979; 85.7%; Pred. No. 1.3e+02; Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABP64908 standard; Protein; 1044 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunostimulant; cerebroprotective.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-NOV-2001; 2001WO-US42950.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-NOV-2000; 2000US-0714936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-FEB-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human protein SEQ ID 568.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-590824/63.
N-PSDB; ABQ99494.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            663 FIHKVHF 669
WPI; 2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
nes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 FLHKVHF 7
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                                                                                                                                                                                                                                                                                                                                                                   979 AA;
                    N-PSDB; ABL07831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200259260-A2.
                                                                                       interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABP64908;
                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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The present invention relates to novel human coding sequences

(ABQ99268-ABQ99608) and proteins (ABP64682-ABP65022). The sequences are

cueful in therapeutic, diagnostic and research methods. The

polynucleotides may be used in the field of molecular biology as

conversely the recombinant production of protein, or in generation of anti-sense

to the recombinant production of protein, or in generation of anti-sense

CC for the recombinant production of protein or in generation of anti-sense

DNA or RNA. The polynucleotides are useful in diagnostics as expressed

sequence tags (ESTs) for identifying expressed genes or for physical

mapping of the human genome. The proteins may be used as molecular weight

cmarkers, or as nutritional sources or supplements. The proteins may be

used to maintain and expand cell population in a totipotential or

cused to maintain and expand cell population in a totipotential or

puriporential state useful for re-engineering damaged or diseased

tissues, transplantation, manufacture of bio-pharmaceuticals or the

cyclophenial state useful for re-engineering damaged or diseased

tissues, transplantation, manufacture of bio-pharmaceuticals or the

cyclophenial proteins or mellorating disorders involving aberrant

contral/peripheral nervous system diseases, mechanical and traumatic

disorders, non-healing wounds, immune descinencies and disorders,

cinfectious diseases caused by viral, bacterial or fungal infection,

disorders, or cancer. The polynucleotide sequences of the invention were

assembled from ESTs isolated mainly by sequencing by hybridisation, and

cassembled from ESTs isolated mainly by sequencing by hybridisation, and

in some cases, sequences obtained from one or more public databases.

Note: The sequence data for this patent did not form part of the printed

cyclopher the polynucleotide sequences of the printed

cyclopher the sequence obtained in electronic format directly from WIPO

cyclopher the protein protein part of the printed

cyclopher the polynucleotide protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human prostate cancer antigen protein sequence SEQ ID NO:973.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75.0%; Score 39; DB 23; Length 1044; 75.0%; Pred. No. 1.4e+02; tive 1; Mismatches 1; Indels C
Claim 20; SEQ ID 568; 394pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB56395 standard; Protein; 102 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-MAR-2000; 2000WO-US05988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .2-MAR-1999; 99US-0124270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     903 FLHKAHFH 910
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 FLHKVHFY 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1044 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200055174-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB56395;
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WPI; 2000-587513/55.

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Appliance to Appliance the following process of a contest accounted accounte
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                                                      Prostate cancer associated gene sequences, referred to as prostate cancer antigens, useful for treatment, prevention, and diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative,
                                                                                                                                                                                                                          AAF15566 to AAF16505 encode the human prostate cancer associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73.1%; Score 38; DB 21; Length 102; 75.0%; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human ORFX protein sequence SEQ ID NO:1422.
                                                                                                                                                                    Claim 11; Page 1413; 2338pp; English.
                                                                                                             disorders such as prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABP00720 standard; Protein; 79 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-2000; 2000US-206132P.
29-AUG-2000; 2000US-228716P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-106308/14.
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4 FEHKLHFY 11
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              102 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    myasthenia gravis.
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N-PSDB; AAF15598.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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The present invertions substantially purinted names in the present invertion users in the present invertion in Sabrol frame, ORFX, where X is 1-11491 process. In the specification). ABN15/52 to ABN27252 encode the human ORFX in the specification). ABN15/52 to ABN27252 encode the human ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating syndrome associated with ORFX-associated disorder. ORFX polymouclectide can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, to psoriasis, benigh tumnours, kebloid, degenerative disorders, lasenorthage, of transplantation, cardiovascular diseases, disorders related to organ transplantation, cardiovascular diseases, disbetes mellitus, systemic cupus exryhematosus, hypertension, hypothyroidism, cholesterol ester storage disease, various immune deficiencies and disorders, infectious disease, autoimmune thyroiditis, myssthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. ORFX proteins are also useful for treating burns, incisions, ulcers, for treating osteoporosis, conceedion or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from cypothic damage.

One degeneration was obtained in electronic format directly from WIPO can fip. int/pub/published_pct_sequences.
                                                                          invention describes substantially purified human proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
hyperproliferative disorders and autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Unsure.
/note= "This amino acid is unknown."
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/note= "This amino acid is unknown."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
                                       Disclosure; SEQ ID 1422; 1037pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR57000 standard; peptide; 25 AA.
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(first entry)
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Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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Gaps

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1; Indels

1; Mismatches

89US-0402695

31-AUG-1989;

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99US-0134218
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29-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAG12473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ^{8} \times ^{9} \times
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                                                                                                                                                                                                                                                                 The histo-blood group ABH determinants are major allogeneic antigens in both erythrocytes and tissues of humans. They generally constitute peripheral parts of the oligosaccharide chains of glycoconjugates i.e.linked to lipids (glycosphingolipids) or to proteins (glycoproteins). It was proposed that the A and B phenotypes were associated with glycosyltransferases that converted the H substance associated with the O phenotype to A and B respectively, through the addition of alphal-3-N-acetylgalactosamine or alphal-3-galactosyl residues to the H antigen Fuc-alphal-2cal-betal-R. Hence, the primary products of the histo-blood group A and B genes are the respectively glycosyltransferases. This is a firagment of the A group transferase. See also AAR$6995-R57010.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated DNA molecules - encode human histo-blood groups A-, B- and O-glycotransferases
                                                                                                                                                                 å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-terminal fragment of human histo-blood group A transferase.
                                                                                                                                                               Isolated DNA molecules - encode human histo-blood groups A-,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69.2%; Score 36; DB 15; Length 25; 71.4%; Pred. No. 11; 0; Indels ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clausen H, Hakomori S, White T, Yamamoto F;
                                                                               White T, Yamamoto F;
                                                                                                                                                                                                                             Example 2; Column 35-36; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR57007 standard; peptide; 37 AA.
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91US-0752101.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 71.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BIOM-) BIOMEMBRANE INST
                                          (BIOM-) BIOMEMBRANE INST
                                                                                    Hakomori S,
                                                                                                                                                                                        and O-glycotransferases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (updated)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1994-217098/26.
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6 HRVHYYV 12
                                                                                                                       WPI; 1994-217098/26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-AUG-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-AUG-1991;
  29-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-MAR-2003
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                                                                                    Clausen H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR57007;
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                                           The histo-blood group ABH determinants are major allogeneic antigens in both erythrocytes and tissues of humans. They generally constitute peripheral parts of the oligosaccharide chains of glycoconjugates i.e.linked to lipids (glycosphingolipids) or to proteins (glycoproteins). It was proposed that the A and B phenotypes were associated with the O phenotype to A and B converted the substance associated with the O phenotype to A and B converted the substance associated with the O phenotype to A and B converted or alphal-3-galactosyl residues to the H antigen Fuc-alphal-2Galberal-R. Hence, the primary products of the histo-blood group A and B genes are the respective glycosyltransferases. This is a firagment of the A group transferase. See also AARS6995-R57010. (Updated on 25-WAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zea mays protein fragment SEQ ID NO: 11599.
Example 2; Column 41-42; 63pp; English.
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26-JUL-1999; 27-JUL-1999; 27-JUL-1999; 27-JUL-1999; 22-JUL-1999; 02-AUG-1999; 02-AUG-1999; 04-AUG-1999; 06-AUG-1999; 06-AUG-1999; 06-AUG-1999; 06-AUG-1999; 113-AUG-1999; 113-AUG-1999; 113-AUG-1999; 113-AUG-1999; 113-AUG-1999; 123-AUG-1999; 123-AUG-1999; 123-AUG-1999; 125-AUG-1999; 27-AUG-1999;	07-SEP-1999; 13-SEP-1999; 15-SEP-1999; 20-SEP-1999; 22-SEP-1999; 24-SEP-1999; 24-SEP-1999; 24-SEP-1999; 26-OCT-1999; 06-OCT-1999; 07-OCT-1999; 13-OCT-1999; 13-OCT-1999; 14-OCT-1999; 14-OCT-1999; 14-OCT-1999; 14-OCT-1999; 14-OCT-1999; 14-OCT-1999; 14-OCT-1999; 14-OCT-1999; 14-OCT-1999; 12-OCT-1999; 12-OCT-1999; 12-OCT-1999; 13-OCT-1999; 14-OCT-1999; 14-OCT-1999; 14-OCT-1999; 14-OCT-1999; 14-OCT-1999; 14-OCT-1999; 12-OCT-1999; 12-OCT-1999; 13-OCT-1999; 14-OCT-1999; 14-OCT-1999; 14-OCT-1999; 14-OCT-1999; 14-OCT-1999; 14-OCT-1999; 14-OCT-1999; 12-OCT-1999; 12-OCT-1999; 13-OCT-1999; 14-OCT-1999; 14-OCT-1999; 14-OCT-1999; 14-OCT-1999; 14-OCT-1999; 14-OCT-1999; 14-OCT-1999; 14-OCT-1999; 14-OCT-1999; 14-OCT-1999; 14-OCT-1999; 14-OCT-1999; 15-OCT-1999; 16-OCT-1999;
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134219. 1344219. 1344760. 1344760. 134576. 135629. 136629. 136629. 136629. 137528.	140699 11440699 114400899 11441828 11441829 11441829 114418 114418 114418 114418 114418 114518 11468
99US - 0134219. 99US - 01342219. 99US - 0134370. 99US - 0134371. 99US - 01343476. 99US - 0135629. 99US - 0135629. 99US - 0135629. 99US - 0135632. 99US - 013722. 99US - 013722. 99US - 013724. 99US - 0137528. 99US - 0137528. 99US - 0137528. 99US - 0139458.	0-SN666
14-MAY-1999; 14-MAY-1999; 18-MAY-1999; 20-MAY-1999; 20-MAY-1999; 21-MAY-1999; 22-MAY-1999; 23-MAY-1999; 24-MAY-1999; 26-MAY-1999; 26-MAY-1999; 26-MAY-1999; 26-MAY-1999; 26-MAY-1999; 26-MAY-1999; 26-MAY-1999; 26-MAY-1999; 26-MAY-1999; 16-UN-1999; 16-UN-1999; 16-UN-1999; 18-UN-1999; 18-UN-1999; 18-UN-1999; 18-UN-1999; 18-UN-1999; 18-UN-1999; 18-UN-1999; 18-UN-1999; 18-UN-1999; 18-UN-1999; 18-UN-1999; 18-UN-1999; 18-UN-1999; 18-UN-1999; 18-UN-1999; 18-UN-1999; 18-UN-1999; 18-UN-1999; 23-UN-1999;	
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21-JUN-1999;
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09-JUL-1999;
12-JUL-1999;
13-JUL-1999;
14-JUL-1999;
15-JUL-1999;
24 - MAY - 1999;
25 - MAY - 1999;
28 - MAY - 1999;
01 - JUN - 1999;
03 - JUN - 1999;
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18-JUN-1999;
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28-JUN-1999;
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01-JUL-1999;
01-JUL-1999;
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22-JUL-1999;
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28-JUL-1999;
02-AUG-1999;
02-AUG-1999;
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23-JUN-1999;
23-JUN-1999;
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  0
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                                                                                                                                                                             Gaps
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0
                                                                                                                                                   Score 36; DB 21; Length 95; Pred. No. 41;
                                                                                                                                                                             1; Indels
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                                                                                                                                                               d. No. 41;
Mismatches
                                                                                                                                                                                                                                                                                                      AAG25910 standard; Protein; 128 AA.
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99US-0123180.
99US-0125788.
99US-0125788.
99US-0125785.
99US-0127462.
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99US-013048.
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99US-0132048.
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99US-013208.
99US-013208.
99US-013208.
99US-013208.
              99US-0161405.
99US-0161360.
99US-0161359.
99US-0161360.
99US-0161361.
99US-0161992.
99US-0161993.
                                                                                                                                                   69.2%;
55.6%;
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    99US-0161404
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74 FVHDLHFFV 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zea mays subsp. mays.
                                                                                                                                                                                                       1 FLHKVHFYV 9
                                                                                                                                                           l Similarity
5, Conserva
 25-0CT-1999;
25-0CT-1999;
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
28-0CT-1999;
28-0CT-1999;
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22-MAR-1999
22-MAR-1999
01-APR-1999
06-APR-1999
06-APR-1999
16-APR-1999
19-APR-1999
23-APR-1999
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30-APR-1999
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05-MAY-1999;
06-MAY-1999;
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14-MAY-1999;
14-MAY-1999;
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14-MAY-1999;
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21-MAY-1999
                                                                                                                                                                                                                                                                                                                                AAG25910;
                                                                                                                                                   Query Match
Best Local S
                                                                                                                                                                                                                                                                         RESULT 12
    AAG25910
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74 FVHDLHFFV 82
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24-MAY-1999;
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Query Match
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Best Local Similarity 55.6%; Pred. No. 72;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps

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23 - 70N - 1999

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FVHDLHFFV 120
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AAG 35416
AAG 3547
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AAC AAC 37
AAC 37
AAC AAC 37
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Blood, group, determinant, antigen, erythrocyte, oligosaccharide; glycoconjugate; glycosphingolipid; glycoprotein; glycosyltransferase; transferase.
                                                                                                                                                                                                                                                                                       Isolated DNA molecules - encode human histo-blood groups A-, B- and O-glycotransferases
                                                                                                                                                                                                                                                Clausen H, Hakomori S, White T, Yamamoto F;
                                                                                                                                          /note= "Site of deletion."
                                                           Partial sequence of human A transferase.
                                                                                                                                                                                                                                                                                                              Example 9; Figure 10; 63pp; English.
                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                        89US-0402695.
91US-0752101.
                                                                                                                                                                                          91US-0752101.
                                      (updated)
(first entry)
                                                                                                                                                                                                                                (BIOM-) BIOMEMBRANE INST.
                                                                                                                                                                                                                                                                WPI; 1994-217098/26.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 195 AA;
                                                                                                                                                                                                                                                                       N-PSDB; AAQ68826.
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29-AUG-1991;
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16-FEB-1995
                                                                                                            Homo sapiens
                                                                                                                                                                                          29-AUG-1991;
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                                                                                                                                                                         05-JUL-1994
                      AAR57024;
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AAR57024
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55.6%;
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The histo-blood group ABH determinants are major allogeneic antigens in both erythrocytes and tissues of humans. They generally constitute peripheral parts of the oligosaccharide chains of glycoconjugates i.e.linked to lipids (glycosphingolipids) or to proteins (glycosphingolipids) or to proteins (glycosphingolipids) or to proteins (glycosphingolipids) or to proteins (glycosphingolipids) or to phenotypes were associated with glycosyltransferases that converted the H substance associated with the Ophenotype to A and B respectively, through the addition of alphal-3-N-acetylgalactosamine or alphal-3-galactosyl residues to the H antigen Fuc-alphal-2Galbetal-R. Hence, the primary products of the histo-blood group A and B genes are the respective glycosyltransferases. The full (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: December 16, 2003, 14:14:27
Job time : 33 secs
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|:| :||:| FVHDLHFFV 82

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Sequence 6, Appli Sequence 18, Appl Sequence 5000, Ap Sequence 2, Appli Sequence 2, Appli Sequence 4499, Ap Sequence 5382, Ap Sequence 14, Appl Sequence 24497, A Sequence 24497, A

Sequence 671, App Sequence 4203, Ap

Sequence 48, Seguence 48,

Sequence 7 Seguence

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/label= unsure
/note= "These amino acids are unknown."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMFUTER: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.25

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/07/752,101A

FILING DATE: 19910829

CLASSIFICATION NUMBER: 32,629

RETORNEY/AGENT INFORMATION:

NAME: Bharkey, Richard G.

REGISTRANCE/DOCKET NUMBER: 32,629

REFERENCE/DOCKET NUMBER: 15036.406C1

TELEPHONE: 206-622-4900

TELEPHONE: 206-622-4900

TELEPHONE: 206-622-4031

INFORMATION FOR SEQ ID NO: 6: SEQUENCE CRRARACTERISTICS:

LEMBYTH: 225 amino acids
US-08-982-493-6
US-09-322-478-18
US-09-134-001C-5000
US-08-696-139-4
US-08-696-139-2
US-07-698-926A-2
US-09-107-532A-4499
US-09-107-532A-4499
US-09-107-532A-4499
US-09-252-994A-24497
US-09-58-4419-313
US-09-58-4419-313
US-09-58-4419-313
US-09-186-188B-48
US-09-186-188B-48
US-09-186-188B-48
US-09-134-001C-4203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B: Seed and Berry
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 1
US-07-752-101A-6
Sequence 6, Application US/07752101A
Patent No. 5326857
GENERAL INFORMATION:
APPLICANT: Yamamoto, Fumi-ichiro
APPLICANT: White, Thayer
APPLICANT: Hakomori, Sen-itiroh
APPLICANT: Clausen, Henrik
TITLE OF INVENTION: ABO GENOTYPING
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 25 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRAGMENT TYPE: N-terminal
  MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Region
LOCATION: 15..16
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                         (without alignments)
30.875 Million cell updates/sec
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                                                                                                                                                                                            December 16, 2003, 14:11:00 ; Search time 12.3333 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Sequence 6, Sequence 6, Sequence 6, Sequence 6, Sequence 8, Sequen
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Sequence 6
Sequence 6
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Sequence 2
Sequence 7
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Sequence
Sequence
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
                            GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-07-752-101A-13
US-07-752-101A-35
US-07-752-101A-35
US-07-752-101A-38
US-07-752-101A-38
US-07-752-101A-38
US-07-752-101A-38
US-07-752-101A-31
US-07-752-101A-51
US-07-752-101A-51
US-07-752-101A-51
US-07-752-101A-51
US-07-752-101A-6
US-08-202-05-6
US-08-801-228-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                     - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                       US-09-870-089B-5
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Match Length DB
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                                                                                                                                                                                                                                                                                                                                                                 Sequence:
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                              69.2%; Score 36; DB 1; Length 25; 71.4%; Pred. No. 4.9; tive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/752,101A
FILING DATE: 19910829
                                                                                                                                                                                                                                                                                                                                                                                                       E: Seed and Berry
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DAME:
CLASSIFICATION:
ATJOANNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 150036.406C1
TELEPHONE: 206-682-6910
TELEPA: 3723836
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                      Sequence 13, Application US/07752101A
Patent No. 5326857
GENERAL INFORMATION:
APPLICANT: Yamamoto, Fumi-ichiro
APPLICANT: White, Thayer
APPLICANT: Hakomori, Sen-itiroh
APPLICANT: Clausen, Henrik
TITLE OF INVENTION: ABO GENOTYPING
NUMBER OF SEQUENCES: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 3
US-07-752-101A-68
Sequence 68, Application US/07752101A
Patent No. 5326857
GENERAL INFORMATION:
APPLICANT: Yamamoto, Fumi-ichiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
                5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 37 amino acid
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and
                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Seattle
STATE: Washington
COUNTRY: U.S.
ZIP: 98104
                                                                                                                            |:||:||
6 HRVHYYV 12
                                                                                                       3 HKVHFYV 9
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3 HRVHYYV 9
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US-07-752-101A-13
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US-07-752-101A-6
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0; Gaps
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                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/752,101A
FILING DATE: 19910829
CLASSIFICATION: 435
                                                                                                                                       ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Seed and Berry
6300 Columbia Center, 701 Fifth Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 150036.406C1
TRIECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Yamamoto, Fumi-ichiro
APPLICANT: White, Thayer
APPLICANT: Hakomori, Sen-itiroh
APPLICANT: Clausen, Henrik
TITLE OF INVENTION: ABO GENOTYPING
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADORESS:
APPLICANT: White, Thayer
APPLICANT: Hakomori, Sen-itiroh
APPLICANT: Clausen, Henrik
TITLE OF INVENTION: ABO GENOTYPING
NUMBR OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 35, Application US/07752101A Patent No. 5326857 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 195 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
US-07-752-101A-68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELERAX: 206-682-6031
TELEX: 3723836
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 6300 Columb
CITY: Seattle
STATE: Washington
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                                                                                                                                                                                                                                  COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 98104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 4
US-07-752-101A-35
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                                                          Query Match 69.2%; Score 36; DB 1; Length 353; Best Local Similarity 71.4%; Pred. No. 60; Matches 5; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69.2%; Score 36; DB 1; Length 354; 71.4%; Pred. No. 60;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/752,101A

FILING DATE: 19910629

CLASSIFICATION: 435

ATTONENY/AGENT INPORMATION:

NAME: SIARKEY, Richard G.

REGISTRATION NUMBER: 32,629

REGISTRATION NUMBER: 32,629

REFERENCE/DOCKET NUMBER: 32,629

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEFRA: 206-682-490

TELEFRA: 206-682-490

TELEFRA: 206-682-4031

TELES: 3723836

INPORMATION FOR SEQ ID NO: 38:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Yamamoto, Fumi-ichiro
APPLICANT: White, Thayer
PREDICANT: Hakomori, Sen-itiroh
APPLICANT: Hacusen, Henrik
TITLE OF INVENTION: ABO GENOTYPING
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSER: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                       US-07-752-101A-38
; Sequence 38, Application US/07752101A
Patent No. 5326857
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-07-752-101A-39
; Sequence 39, Application US/07752101A
; Patent No. 5326857
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 354 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Seattle
STATE: Washington
COUNTRY: U.S.
ZIP: 98104
                                                                                                                                                                                |:||:||
144 HRVHYYV 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |:||:||
145 HRVHYYV 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 HKVHFYV 9
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    ; FRAGMEN 1111.
US-07-752-101A-36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/752,101A
FILING DATE: 19910829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5: Seed and Berry
6300 Columbia Center, 701 Fifth Avenue
                                                                             ATTORNEY AGENT INPORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 150036.406C1
TELECOMMUNICATION INPORMATION:
TELEFONE: 206-622-4900
TELEFAX: 206-682-6031
TELEFAX: 3723836
INPORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENOTH: 353 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 15036,406C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
TELEPACE 206-682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 36, Application US/077E2101A
Fatent No. 5326857
GENERAL INFORMATION:
APPLICANT: Yamamoto, Fumi-ichiro
APPLICANT: White, Thayer
APPLICANT: Hakomori, Sen-itiroh
APPLICANT: Clausen, Henrik
TITLE OF INVENTION: ABO GENOTYPING
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 F.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/752,101A
FILING DATE: 19910829
CLASSIFICATION: 435
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELERAX: 206-682-6031
TELEX: 3723836
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 353 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 71.4.
5. Conservative
                                                                                                                                                                                                                                                                                                                                   ; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-752-101A-35
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MOLECULE TYPE: peptide
HYPOTHETICAL: NO
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144 HRVHYYV 150
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US-07-752-101A-36
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69.2%; Score 36; DB 1; Length 354;
Best Local Similarity 71.4%; Pred. No. 60;
Matches 5; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/752,101A
FILING DATE: 19910829
CLASSIFICATION: 435
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STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
                                                                                                                                                      ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: Sharkey, Richard G.
RAGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 150036.406C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
TELEPHONE: 206-682-6031
TELER: 3723836
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 354 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 41, Application US/07752101A
Patent No. 5326857
GENERAL INFORMATION:
APPLICANT: Yamamoto, Fumi-ichiro
APPLICANT: White, Thayer
APPLICANT: Hakenori, Sen-itiroh
APPLICANT: Clausen, Henrik
TITLE OF INVENTION: ABO GENOTYPING
NUMBER OF SEQUENCES: 69
CORRESPONDENCE Seed and Berry
APPLICANT: Yamamoto, Fumi-ichiro
APPLICANT: White, Thayer
APPLICANT: Hakomori, Sen-itiroh
APPLICANT: Clausen, Henrik
TITLE OF INVENTION: ABO GENOTYPING
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: Linea.
MOLECULE TYPE: peptide
                                                                                                                                                                        STREET: 6300 Columi
CITY: Seattle
STATE: Washington
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US-07-752-101A-39
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US-07-752-101A-41
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Query Match 69.2%; Score 36; DB 1; Length 354; Best Local Similarity 71.4%; Pred. No. 60; Matches 5; Conservative 2; Mismatches 0; Indels
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MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DoS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/752,101A
FILING DATE: 1991029
CLASSIFICATION: 435
ATVONEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REGISTRATION NUMBER: 32,629
REGISTRATION NUMBER: 32,629
TELEFONE: 206-622-490
TELEFRAX: 206-622-490
TELEFRAX: 206-622-490
TELERY: 3733836
INFORMATION FOR SEQ ID NO: 51:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 51, Application US/07752101A

Patent No. 5326857

GENERAL INFORMATION:
APPLICANT: Yamamoto, Fumi-ichiro
APPLICANT: White, Thayer
APPLICANT: White, Thayer
APPLICANT: Hakomori, Sen-itiroh
APPLICANT: Clausen, Henrik
TITLE OF INVENTION: ABO GENOTYPING
NUMBER OF SEQUENCES: 69
CORRESPONDENCES: 69
CORRESPONDENCE ADDRESSE:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
SOFTWARE: Patentin Release #1.0, Version #1.25
     CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/752,101A
FILING DATE: 19910829
CLASSIFTCATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 150036,406C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-582-4900
TELEPHONE: 206-582-6031
TELEFAX: 206-682-6031
TELEFAX: 3723336
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 354 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 354 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 6300 Colum
CITY: Seattle
STATE: Washington
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145 HRVHYYV 151
                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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ZIP: 98104
                                                                                                                                                                                                                                                                                                                                                                                   TYPE: AMINO A STRANDEDNESS:
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US-07-752-101A-51
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0; Gaps
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Sequence 5, Application US/08202056

Patent No. 5440021

GENERAL INFORMATION:

APPLICANT: Chuntharapai, Anan

APPLICANT: Kim, Kyung Jin

APPLICANT: Kim, Kyung Jin

APPLICANT: Lee, James

TITLE OF INVENTION: Antibodies to Human IL-8 Type B Receptor

WHERE OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67.3%; Score 35; DB 1; Length 372; 85.7%; Pred. No. 94;
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Patent No. 5543503
GENERAL INFORMATION:
APPLICANT: Chuntharapai, Anan
APPLICANT: Lee, James
APPLICANT: Hebert, Caroline
APPLICANT: Jin Kim, K.
TITLE OF INFORMATION: Antibodies to Human PF4A Receptors
NUMBER OF SEQUENCES: 6
CORRESCONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: 18M PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genentech) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/202,056 FILING DATE: 25-FEB-1994 CLASSIFICATION NUMBER: 07/67211 APPLICATION NUMBER: 07/67211 ATTORNEY ABPLICATION NUMBER: 07/67211 ATTORNEY ABPLICATION NUMBER: 07/67211 ATTORNEY ABPLICATION NUMBER: 39-MAR-1991 NAMB: LOVE, RICHARD B. REGISTRATION NUMBER: 34,659
                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3: Genentech, Inc.
460 Point San Bruno Blvd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 70
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IELEKA: 910/371-7168
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
IENGTH: 372 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 85./*,
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 415/225-5530
415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
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145 HRVHYYV 151
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128 LHKVNFY 134
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US-08-202-056-5
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/note= "These amino acids are unknown."
                                                                                                                                                            69.2%; Score 36; DB 1; Length 354; 71.4%; Pred. No. 60; tive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 36; DB 1; Length 375;
Pred. No. 64;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/752,101A
FILING DATE: 19910829
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REGISTRATION NUMBER: 32,629
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAK: 206-682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Yamamoto, Fumi-ichiro
APPLICANT: White, Thayer
APPLICANT: Hakomori, Sen-itiroh
APPLICANT: Clausen, Henrik
TITLE OP INVENTION: ABO GENOTYPING
NUMBER OF SEQUENCES: 69
                                                                                                                                                                                                                                                                                                                                                    RESULT 10
US-07-752-101A-52
Sequence 52, Application US/07752101A
Patent No. 5326857
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 372336
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
IENGTH: 375 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sh 69.2%;
Similarity 71.4%;
5; Conservative 2
                                                       HYPOTHETICAL: NO ANTI-SENSE: NO FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FRAGMENT TYPE: N-terminal
                                                                                                                                                                                     Best_Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
TOPOLOGY: linear
STRANDEDNESS: single
                                   MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Region
LOCATION: 1..53
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                         |:||:||
145 HRVHYYV 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 5; Conserva
                   linear
                                                                                                                                                                                                                                                3 HKVHFYV 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98104
                                                                                                          ; FRAGMENT TYPE
US-07-752-101A-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-07-752-101A-52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                   Query Match
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APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/67211
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 34,659
REFRENENCE/DOCKET NUMBER: 706P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-981
TELER: 910/371-7168
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
TYPE: Amino Acid
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 85./*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||||:||
128 LHKVNFY 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 LHKVHFY 8
                                                                                                                                                                                                                                                                                                                                                                                                          US-08-701-265-6
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US-08-284-586-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 85.7%; Pred. No. 94;
Matches 6; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Chuntharapai, Anan
APPLICANT: Lee, James
APPLICANT: Lee, James
APPLICANT: Jin Kim, K.
TITLE OF INVENTION: Antibodies to Human PF4A Receptors
NUMBER OF SUCURNES: 6
CORRESPONDENCE ADDRESS:
                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 1BM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Winderin (Genentech)
CURRENT APPLICATION DATA:
PFLICATION NUMBER: US/08/076,093A
FILING DATE: 11-Jun-1993
CLASSIFICATION NUMBER: 05/08/076,093A
FILING DATE: 11-Jun-1993
CLASSIFICATION DATA: APPLICATION DATA: APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
PRIOR APPLICATION NUMBER: 34,659
FILING DATE: 29-MAR-1991
ATTORNEY AGENT INFORMATION:
APPLICATION NUMBER: 34,659
REGISTRATION NUMBER: 34,659
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 706P2
TELECOMMUNICATION INFORMATION:
TELEPRONE: 415/25-5530
TELERY: 415/25-981
TELERY: 410/371-7168
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: Insh PC compatible
COMPUTER: Insh PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/701,265
FLING DATE: 22-AUG-1996
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 22-AUG-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/076093
FILING DATE: 11-Jun-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-701-265-6; Sequence 6, Application US/08701265; Patent No. 5776457
         South San Francisco : California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 372 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128 LHKVNFY 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 LHKVHFY 8
                                                      USA
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Gaps
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                                                                                                                                                                                                                                                                  Sequence 6, Application US/08284586;
Sequence 6, Application US/08284586;
Patent No. 5840856
GENERAL INFORMATION:
APPLICANT: Chuntharapai, Anan
APPLICANT: Lee, James
APPLICANT: Hebert, Caroline
APPLICANT: Hebert, Caroline
APPLICANT: Hobert, Caroline
APPLICANT: An kim, K.
TITLE OF INVENTION: Antibodies to Human PF4A Receptors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADRESS:
ADDRESSEE: Genencech, Inc.
STREET: 460 Point San Bruno Blvd
STREET: California
COUNTRY: USA
67.3%; Score 35; DB 1; Length 372; 85.7%; Pred. No. 94; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 1BM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinhPatin (Genentech) CURENT APPLICATION DATA: APPLICATION NUMBER: US/08/284,586 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION UNBER: 05/00/06,093A

FILING DATE: 11-Jun-1993

APPLICATION NUMBER: 07/810782

FILING DATE: 19-DEC-1991

PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: 19-DEC-1991

ATTORNATION NUMBER: 07/677211

ATTORNAY AGENT INFORMATION:

NAME: LOVE, RICHARD B

REFERENCE/DOCKET NUMBER: 706P2

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELERENCE 101/25-550

TELERA: 910/371-7168

INFORMATION FOR SEQ ID NO: 6:
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                                                                                                                                                      Query Match 67.3%; Score 35; DB 2; Length 372; Best Local Similarity 85.7%; Pred. No. 94; Matches 6; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/08805478

Sequence 6, Application US/08805478

Sequence 6, Application US/08805478

Senent No. 5874543

APPLICANT: Chuntharapai, Anan
APPLICANT: Lee, James
APPLICANT: Lee, James
APPLICANT: Lee, James
APPLICANT: Hebert, Caroline
APPLICANT: Hebert, Caroline
APPLICANT: Hebert, Saling K.

TITLE OF INVENTION: ANTIBODIES TO PF4A RECEPTOR
NUMBER OF SEQUENCES:
CORRESPONDENCES:
CORRESPONDENCES:
STREET: 460 Point San Bruno Blvd
STREET: 460 Point San Bruno Blvd
STREET: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USAR

ZIP: 94080
COMPUTER READABLE FORM:
REDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 125 inch, 1.44 Mb floppy disk
COMPUTER: SIS inch, 1.44 Mb floppy disk
COMPUTER: WinFatin (Genentech)
SORTWARE: WinFatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/805,478
FILING DATE: 25-Feb-1997
CLASSIFICATION NUMBER: 08/784586
FILING DATE: 10-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/76093
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
ATTORNEY/ACENT NUMBER: 94/659
REFERENCE/DOCKET NUMBER: 94/659
REPERENCE/DOCKET NUMBER: 90706P2PICI
TELEPHONE: 415/952-9881
FILEPHONE: 910/311-7168
INFORMATION FOR SEG ID NO: 6:
SEQUENCE CHARACTERISTICS:
INFORMATION CACIET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LENGTH: 372 amino acids; TYPE: Amino Acid ; TOPOLOGY: Linear US-08-805-478-6
; SEQUENCE CHARACTERISTICS:
; LENGTH: 372 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-284-586-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||||:||
128 LHKVNFY 134
                                                                                                                                                                                                                                                                                                         128 LHKVNFY 134
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US-08-805-478-6
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Search completed: December 16, 2003, 14:20:39 Job time : 12.3333 secs
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Sequence 107, App
Sequence 973, App
Sequence 3, Appli
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Sequence 6647, Ap
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Sequence 9, Appli
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                                                                                                                                                 December 16, 2003, 14:18:11; Search time 22.1667 Seconds (without alignments) 75.512 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Published Applications AA:*

1: /cgn2_6/ptodatca/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodatca/2/pubpaa/PCT_NBW_PUB_pep:*
3: /cgn2_6/ptodatca/2/pubpaa/USO6_NEW_PUB_pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                    OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0% Maximum Match 100%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                length: 0
length: 2000000000
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52
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Match Length DB
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Maximum DB seq
                                                                                                                                                                                                                                                                                  Perfect score:
                                                                                                                                                                                                                                                                                                                                                       Scoring table:
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                                                                                                                                                                                                                                                                                                          Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                 Searched:
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                                                                                                                                                      Run on:
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US-09-738-626-6647
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Sequence 12, Appl
Sequence 5, Appl
Sequence 13, Appl
Sequence 14, Appl
Sequence 11311, A
Sequence 11311, A
US-09-870-089B-5

US-09-738-626-6647

US-09-870-089B-11

US-09-870-089B-9

US-10-015-115-107

US-09-925-300-973

US-09-995-419A-11

US-09-995-419A-11

US-09-995-419A-13

US-09-995-419A-13

US-09-995-419A-13

US-09-815-242-11490

US-09-815-242-11490

US-09-895-913A-298
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Sequence 298, App

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Sequence 6, Appli
Sequence 10, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 17, Appli
Sequence 17, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
                              Sequence 60, Appl
Sequence 4446, Ap
Sequence 13494, A
Sequence 1, Appli
                                                             Sequence 139, App
Sequence 18, Appl
Sequence 273, App
Sequence 640, Appl
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                                                                                                                                                                                      27, Appl
17, Appl
7, Appli
                                                                                                                                                                                                           Sequence 4433, Ap
Sequence 172, App
Sequence 1039, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                      Sequence 27
Sequence 17
  Sequence
                 Sequence
                         Sequence
                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                 Sequence 5/ Application US/09970009B; Publication No. US20030175252A1; GENERAL AIRCRANTION: APPLICATION NO. US2003175252A1; GENERAL AIRCRANTION: TITLE OF INVENTION: THERAPEUTIC COMPOUNDS FOR OVARIAN CANCER FILE REFERENCE: 68126801209900; CURRENT FILION NUMBER: US/09/870,089B; CURRENT FILION DATE: 2001-05-30; MUMBER OF SEQ ID NOS: 14; SEQ ID NO 5: LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                              ·,
                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 52; DB 12; Length 9; 100.0%; Pred. No. 6.1e+05; Ative 0; Mismatches 0; Indels
US-09-764-869-1039
                                                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6647, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: ATF4/CREB-2 US-09-870-089B-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: NIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 FLHKVHFYV
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                                                                             US-09-870-089E-5
          TYPE: PRT
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SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 9 LANGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 107, Application US/10015115; Publication No. US20030207800A1; GENERAL INFORMATION:
APPLICANT: Shenoy, Suresh G
APPLICANT: Shenoy, Suresh G
APPLICANT: Spytek, Kimberly A
APPLICANT: Patturajan, Meera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) ORGANISM: Drosophila melanogaster US-10-015-115-107
                                                                                                                         ) OTHER INFORMATION: ATF4/CREB-2
US-09-870-089B-9
                                                                TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Guo, Xiaojia
Kekuda, Ramesha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 85.78
Matches 6; Conservative
                                                                                                                                                                                                                                                                       1 FLHKVHFYV 9
                                                                                                                                                                                                                                                                                                               1 FLHKWHWYV 9
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                                                                                                          FEATURE:
                                              LENGTH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11, Application US/09870089B

Publication No. US20030175252A1

GENERAL INFORMATION:
APPLICANT: Charles A. Nicolette
1 TITLE OF INVENTION: THERAPEUTIC COMPOUNDS FOR OVARIAN CANCER
FILE REFERENCE: 68126881209900
CURRENT APPLICATION NUMBER: US/09/870,089B
CURRENT FILING DATE: 2001-05-30
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Charles A. Nicolette
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS FOR OVARIAN CANCER
FILE REPERENCE: 68126881209900
CURRENT APPLICATION NUMBER: US/09/870,089B
CURRENT FILING DATE: 2001-05-30
NUMBER OF SEQ ID NOS: 14
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Query Match

Pest Local Similarity 77.8%; Pred. No. 6.1e+05;

Matches 7; Conservative 1; Mismatches 1; Indels
                                                                                                                                       FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: UP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
                                                                                                                         TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/09870089B
Publication No. US20030175252A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: ATF4/CREB-2
US-09-870-089B-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
                      YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
OZAKI, AKIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 77.5.
Fig. Conservative
    OCHIAI, KEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 FLHSAHFYV 30
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US-09-870-089B-11
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LENGTH: 1043
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US-09-870-089B-9
    APPLICANT:
                                                                  APPLICANT:
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APPLICANT: Shimkets, Richard A
APPLICANT: Taupler, Raymond J
APPLICANT: Taupler, Raymond J
APPLICANT: Li, Li
APPLICANT: Padigaru, Muralidhara
TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
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85.7%; Pred. No. 1.2e+02;
Live 1; Mismatches 0; Indels
Query Match 76.9%; Score 40; DB 12; Length 9; Best Local Similarity 77.8%; Pred. No. 6.1e+05; Matches 7; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE REFERENCE: 12402-211
CURRENT APPLICATION NUMBER: US/10/015,115
CURRENT FILING DATE: 2002-09-23
FRIOR APPLICATION NUMBER: 0/248,153
PRIOR APPLICATION NUMBER: 60/249,153
PRIOR PILING DATE: 2000-11-13
PRIOR FILING DATE: 2001-11-17
PRIOR FILING DATE: 2001-01-26
PRIOR FILING DATE: 2001-01-26
PRIOR FILING DATE: 2001-02-6
PRIOR FILING DATE: 2001-02-6
PRIOR FILING DATE: 2001-02-06
PRIOR FILING DATE: 2001-02-06
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: 60/313,283
PRIOR APPLICATION NUMBER: 2001-07-31
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RESULT 9
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APPLICANT: Geron Corporation
APPLICANT: Schiff, J. Michael
TITLE OF INVENTION: GLYCOSYLTRANSFERASE VECTORS FOR TREATING CANCER
FILE REFERENCE: 083,002
CURRENT APPLICATION NUMBER: US/09/994,427A
CURRENT FILING DATE: 2002-02-26
PRIOR APPLICATION NUMBER: 60/253,395
PRIOR FILING DATE: 2000-11-27
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.1
                        Sequence 973, Application US/09925300
; Batent No. US20020151681A1
; GBNERAL INPORMATION:
; APPLICANT: Craig Rosen,
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR PILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR PILING DATE: 1999-03-12
; NUMBER OF ECO ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 973
...ENGTH: 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 73.1%; Score 38; DB 10; Length 102; Best Local Similarity 75.0%; Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
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US-09-995-419A-11
Sequence 11, Application US/09995419A
FUDIICATION OF US20330032187A1
GENERAL INFORMATION:
APPLICANT: Genome Corporation
APPLICANT: Gold, Joseph D.
APPLICANT: Schiff, J. Michael
TITLE OF INVENTION: 096,004 - SeqList
FILE REFERENCE: 096,004 - SeqList
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 3, Application US/09994427A; Patent No. US20020128221A1; GENERAL INFORMATION:
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Best Local Similarity 71.3.
Best Local Si Conservative
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; ORGANISM: Homo sapiens
US-09-994-427A-3
                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
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144 HRVHYYV 150
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RESULT 6
US-09-925-300-973
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US-09-994-427A-3
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LENGTH: 353
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APPLICANT: Geron Corporation
APPLICANT: Denning, Chris
APPLICANT: Denning, Chris
APPLICANT: Clark, A. John
APPLICANT: Clark, J. Michael
TITLE OF INVENTION: Animal Tissue with Carbohydrate Antigens Compatible for Human
TITLE OF INVENTION: Transplantation and a Carbohydrate Determinant Selection System
TITLE OF INVENTION: Recombination
TITLE OF INVENTION: Recombination
FILE REFERENCE: 731/002
CURRENT APPLICATION NUMBER: US/10/105,963
CURRENT FILING DATE: 2002-03-21
PRIOR PELLOR DATE: 2001-03-21
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APPLICANT: Geron Corporation
APPLICANT: Schiff, J. Michael
TITLE OF INVENTION: GLYCOSYLTRANSFERASE VECTORS FOR TREATING CANCER
FILE REFERENCE: 2002-02-26
CURRENT FILING DATE: 2002-02-26
PRIOR APPLICATION NUMBER: 60/253,395
PRIOR PLING DATE: 2000-11-27
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69.2%; Score 36; DB 15; Length 353; 71.4%; Pred. No. 1.6e+02;
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CURRENT APPLICATION NUMBER: US/09/995,419A CURRENT FILING DATE: 2001-11-26 PRIOR APPLICATION NUMBER: 60/253,357 PRIOR FILING DATE: 2000-11-27 NUMBER OF SEQ ID NOS: 20 SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 12, Application US/10105963; Publication No. US20030068818A1
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SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 71.4
Matches 5; Conservative
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LENGTH: 353
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                        SEQ ID NO 11
LENGTH: 353
TYPE: PRT
ORGANISM: Homo sapiens
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144 HRVHYYV 150
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LENGTH: 354
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Gaps
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APPLICANT: Oblean, Kari L.
APPLICANT: Oblean, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Tradick, John D.
APPLICANT: Tradick, John D.
APPLICANT: Tradick, John D.
APPLICANT: Tamanoto. Robert T.
APPLICANT: Xu, H. Howard
ITLE OF INVENTION: Identification of Essential Genes in
ITLE OF INVENTION: Identification of Essential Genes in
ITLE OF INVENTION: LITTAN. 011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-25
PRIOR PLILING DATE: 2000-05-26
PRIOR PLILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR PLILING DATE: 2000-10-23
PRIOR PLILING DATE: 2000-10-23
PRIOR PLILING DATE: 2000-11-27
PRIOR PLILING DATE: 2000-12-22
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APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 11490, Application US/09815242
; Patent No. USZ0020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
                                                                                                                                                                                                                                                                Sequence 11311, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Hagelbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ohlsen, Kari L.
Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wall, Daniel
Trawick, John D.
Carr, Grant J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 62.59
Matches 5; Conservative
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                                                                               145 HRVHYYV 151
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3 HKVHFYV 9
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LENGTH: 371
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US-10-105-963-14

Sequence 14, Application US/10105963

Publication No. US20030068818A1

GENERAL INFORMATION:
APPLICANT: Geron Corporation
APPLICANT: Denning, Chris
APPLICANT: Clark, A. John
APPLICANT: Clark, A. John
APPLICANT: Clark, A. John
TITLE OF INVENTION: Arimal Tissue with Carbohydrate Antigens Compatible for Human
TITLE OF INVENTION: Arimal Tissue with Carbohydrate Determinant Selection System
TITLE OF INVENTION: Recombination
TITLE OF INVENTION: Recombination
FILE REFERENCE: 731/002

CURRENT APPLICATION NUMBER: US/10/105,963

CURRENT APPLICATION NUMBER: US 60/277,811

PRIOR PILING DATE: 2001-03-21

NUMBER OF SEQ ID NOS: 40

SOFTWARE: PatentIn version 3.1

SEQ ID NO 14

LENGTH: 354
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                                                                                                                 Query Match 69.2%; Score 36; DB 10; Length 354; Best Local Similarity 71.4%; Pred. No. 1.6e+02; Matches 5; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-995-419A-13
US-09-995-419A-13
Sequence 13, Application US/09995419A
Sequence 13, Application No. US20030032187A1
GENERAL INFORMATION:
APPLICANT: GENER CONDERATION
APPLICANT: Gold, Joseph D.
APPLICANT: Gol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
        ORGANISM: Homo sapiens
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                         ; UKGANISM: DO.
US-09-994-427A-5
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Sequence 298, Application US/09895913A

| Sequence 298, Application US/09895913A
| Sequence 298, Application US/09895913A
| Patent No. US20020160456A1
| GENERAL INFORMATION:
| APPLICANT: Kleanthous, Harold
| APPLICANT: Miller, Charles
| APPLICANT: Tomb, Jean Francois
| APPLICANT: Tomb, Jean Francois
| APPLICANT: Order Invention: Identification of Polynucleotides
| APPLICANT: Order Invention: Identification of Polynucleotides
| TITLE OF INVENTION: Identification of Polynucleotides
| TITLE OF INVENTION: Genome
| TITLE OF INVENTION: Genome
| FILE REFERENCE: 06132/043002
| CURRENT FILING DATE: 2001-06-29
| PRIOR FILING DATE: 1997-06-29
| PRIOR PLING DATE: 1997-06-24
| NUMBER OF SEQ ID NOS: 368
| SOFFTAME: PASESEQ for Windows Version 4.0
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-24
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-23
PRIOR PRICH DATE: 2000-11-27
PRIOR PRICH DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PLING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SEQ ID NO 11490
SEQ ID NO 11490
LENGTH: 371
TYPE: PRT
TYPE
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LENGTH: 311
TYPE: PRT
ORGANISM: Helicobacter pylori
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

December 16, 2003, 14:10:15; Search time 10.333 Seconds (without alignments) 83.760 Million cell updates/sec Run on:

US-09-870-089B-5 1 FLHKVHFYV 9 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 segs, 96168682 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_76:*
1: pir1:*
3: pir2:*
5: pir3:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

acyl-CoA thioleste G protein-coupled G protein-coupled hypothetical prote hypothetical prote hypothetical prote hypothetical prote probable DNA repai hypothetical prote hypothetical prote probable regulator hypothetical prote MDCR15 protein - h queuine tRNA-ribos tRNA-guanine trans sensory box/GGDEF endostyle-specific non-heme iron-cont hypothetical prote hypothetical prote hypothetical prote glycoprotein-fucos glycoprotein-fucos cytochrome-c oxida 4-coumarate-CoA li self-incompatibili hypothetical prote protein-coupled hypothetical Description SUMMARIES A82428 T00094 A90546 B95183 G71613 T19691 T46126 T46104 S56162 C71952 T03390 841450 JC5644 AH0655 T32200 A64555 T22697 Query Match Length DB 139 159 178 178 69.2 67.3 67.3 67.3 4.2665.4 4.2665.4 4.2665.4 4.2665.4 Score Result

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metal-regulated pr proteinase 1, mito	hypothetical prote probable phosphate	עב	hypothetical prote	probable c-4 metny probable Lambda CI		B. subtilis YKTP p hymothetical profe	conserved hypothet	hypothetical prote	diaminopimelate de	oligoendopeptidase
G69660 S16817	T27466 B72757	H81391 T05665	T15451	T38986 A71365	AC1199	AI1556	AH3202	T23899	139877	G83758
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153	229	253	265	300	343	343	368	430	432	585
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30 31	33 33	34 35	36	37	39	4.4	4 4	43	44	45

ALIGNMENTS

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A;Nap position: 1
A;Introns: 34/2; 54/2; 197/3; 283/3; 323/3; 384/1; 404/3; 452/2; 493/2; 538/2; 591/1
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                                                                                                                                                                                                                                                          A, Accession: T22794
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Nolecule type: DNA
A;Residues: 1-660 -WILA
A;Residues: 1-660 -WILA
A;Cross-references: EMBL:281553; PIDN:CAB04490.1; GSPDB:GN00019; CESP:F56H6.1
A;Experimental source: clone F56H6
                                                                  C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T22794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 71.2%; Score 37; DB 2; Length 660; Local Similarity 62.5%; Pred. No. 41; es 5; Conservative 3; Mismatches 0; Indels
                                                  hypothetical protein F56H6.1 - Caenorhabditis elegans
                                                                                                                                                                    R;Kershaw, J. submitted to the EMBL Data Library, November 1996 A;Reference number: 219617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 FLHKVHFY &
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RESULT 1
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620 FLHKIYFF 627 ð q

hypothetical frotein YLL065w - yeast (Saccharomyces cerevisiae) RESULT 2

Nilternate names: hypothetical protein 10536
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevision 12-May-1995 #text_change 20-Jun-2000
C;Accession: S50955; S64817
R;Wedler, H.; Wambutt, R.
R;Wedler A, Accession: S50955

A,Cross-references: EMBL:Z47973; NID:g642313; PIDN:CAA87992.1; PID:g642319
R;Wedler, H.; Wedler, E.; Scharfe, M.; Wambutt, R.
Bumitted to the Protein Sequence Database, May 1996
A;Reference number: S64792
A;Accession: S64817 A; Molecule type: DNA A; Residues: 1-116 < WED>

A,Molecule type: DNA A,Residues: 1-116 <WEM> A,Cross-references: EMBL:Z73170; NID:g1360279; PIDN:CAA97519.1; PID:g1360280; MIPS:YLL06 A,Experimental source: strain S288C

```
C'Accession: T46104

RiAlcaraz, J.P.; Clabault, G.; Cottet, A.; Mache, R.; Mewes, H.W.; Lemcke, K.; Mayer, K.: submitted to the Protein Sequence Database, January 2000
A;Reference number: Z23021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Superfamily: histo-blood group I transferase
C;Keywords: glycoprotein; glycosyltransferase; Golgi apparatus; hexosyltransferase; polyr
E;1-11/Domain: intracellular #status predicted <INT>
F;1-2/7/Domain: transmembrane #status predicted <IMM>
F;38-353/Domain: trans-Golgi network lumenal #status predicted
F;12/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein T2J13.120 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Jate: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
C;Accession: T46126
R;Riseger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Mewes, H.W.; Mayer, Ksubmitted to the Protein Sequence Database, November 1999
                                                                                                                                                                                                                                                                                              A;Residues: 145-154, P',156-333 <KOM>
C;Comment: This enzyme forms group A blood type determinants from H antigen determinants
minor subtypes, for example A2 (see PIR:PC1120). Inactive alleles are responsible for gr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Complex: homodimer
C;Function:
A;Description: transfers N-acetylgalactosamine from UDP-N-acetylgalactosamine to glycopro
A; Molecule type: protein
A; Molecule type: protein
A; Residues: X, 65-73, 1S', 76-77 < NAV>
A; Residues: X, 65-73, 1S', 76-77 < NAV>
A; Rominato, Y; McNeill, P.D.; Yanamoto, M.; Russell, M.; Hakomori, S.; Yanamoto, F.
Biochem. Biophys. Res. Commun. 189, 154-164, 1992
A; Title: Animal histo-blood group ABO genes.
A; Reference number: PC1164; MUID:93080551; PMID:1449469
A; Reference number: PC1164; MUID:93080551; PMID:1449469
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 28-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: GDB:118956; OMIM:110300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:AL132967
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Map position: 9q34.1-9q34.2
C;Complex: homodimer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             144 HRVHYYV 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                168 LYKVHFY 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Map position: 3
A;Introns: 5/2; 290/3
A;Note: T2J13.120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                glycoprotein-fucosylgalactoside alpha-N-acetylgalactosaminyltransferase (EC 2.4.1.40) A2 N.Alternate names: histo-blood group A2 transferase (Species: Homo sapiens (man) (Species: Homo sapiens (man) (Species: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 03-Jun-2002 (Spacession: PC1120 (Spacession: PC1120 PC1120 (Spacession: PC1120 P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A.Title: Molecular genetic basis of the histo-blood group ABO system.

A.Reference number: S09593; MUD: 90238543; PMID: 2333095

A.Reference number: S09593

A.Accession: S09593

A.Accession: S09593

A.Reference number: S09593

A.Reference number: S09593

A.Reference number: S13308

A.Residues: 1-353 «YAM2»

A.Residues: 1-353 «YAM2»

B.Sochem. J. 271, 93-98, 1990

A.Title: Purification, properties and partial amino acid sequence of the blood-group-A-g

A.Reference number: S13173; MUD: 91024951; PMID: 2121135
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A;Residues: 1-295 <YAM>
A;Residues: 1-295 <YAM>
A;Cross_references: GB:S44054; NID:g255066; PIDN:AAB23167.1; PID:g255067
C;Superfamily: histo-blood group 1 transferase
C;Keywords: glycosyltransferase; hexosyltransferase
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A;Residues: 1.353 <YAM1>
A;Residues: 1.353 <YAM1>
A;Cross-references: GBs.J05175; NID:g340077; PIDN:AAA36792.1; PID:g340078
R;Yamamoto, F.I.; Clausen, H.; White, T.; Marken, J.; Hakomori, S.I.
Nature 345, 229-233, 1990
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                                                                                                                                                                                        69.2%; Score 36; DB 2; Length 116; 75.0%; Pred. No. 11; tive 0; Mismatches 2; Indels
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A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71.4%; Pred. No. 28; tive 2; Mismatches
        C;Genetics:
A;Gene: SGD:GIN11
A;Coss-references: SGD:S0003988; MIPS:YLL065w
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                                                                                                                                                                                                                                Local Similarity 75.0
nes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             46 FTHKVHHY 53
                                                                                                                                                                                                                                                                                                                                               1 FLHKVHFY 8
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A;Status: preliminary
                                                                                                                          A; Map position: 12L
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 08-Oct-1999
C;Accession: S56162
R;Barella, L.; Loetscher, M.; Tobler, A.; Baggiolini, M.; Moser, B.
Biochem. J. 309, 773-779, 1995
A;Title: Sequence variation of a novel heptahelical leucocyte receptor through alternatify. A;Reference number: S56162; MUID:95366951; PMID:7639692
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A,Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K., A,Title: Complete genome sequence of a multiple drug resistant Salmonella enterica seron A,Reference number: ABOSO2; MUID:21534947; PMID:11677608
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                                                                                                                                                                                                                                                         A.Status: preliminary
A.Modeoule type: DNA
A.Residues: 1-250 cPAR>
A.Cross-references: GB:AL513382; PIDN:CAD08427.1; PID:g16502470; GSPDB:GN00176
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C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T32200
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C;Superfamily: vertebrate rhodopsin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 67.3%; Score 35; DB 2; Length 250; Best Local Similarity 71.4%; Pred. No. 36; Matches 5; Conservative 2; Mismatches 0; Indels
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Ajbescription: The sequence of C. elegans cosmid T02Bll.
A;Reference number: 221135
A;Accession: T32200
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85.7%; Pred. No.
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A;Introns: 47/3; 69/1; 92/1; 180/2
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Best Local Similarity
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A,Gene: STY1347
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probable regulatory protein STY1347 [imported] - Salmonella enterica subsp. enterica ser C;Species: Salmonella enterica subsp. enterica serovar Typhi
C;Species: Almonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AH0655
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A,Residues: 1-512 < vAL.

A,Fesidues: 1-512 < vAL.

A,Cross-references: BMBL:X68067; NID:9505262; PIDN:CAA48806.1; PID:9578437

R;Perez, M.L.; Valverde, J.R.; Batuecas, B.; Amat, F.; Marco, R.; Garesse, R.

B, Mol. Byol. 38, 156-168, 1994

A,Title: Speciation in the Artemia genus: mitochondrial DNA analysis of bisexual and par

A,Reference number: S60624; MUID:94223692; PMID:8169960
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F;9455/Domain: cytochrome-c oxidase chain I homology <COl>
F;9455/Domain: cytochrome-c oxidase chain I homology <COl>
F;59,376/Binding site: here a iron (His) #status predicted
F;238,288,289/Binding site: copper (His) #status predicted
F;238-242/Cross-link: 1'-histidyl-7'-tyrosine (His-Tyr) #status predicted
F;245/Binding site: oxygen (Tyr) #status predicted
F;366/Binding site: magnesium (His) (#barcd with chain II) #status predicted
F;374/Binding site: heme a3 iron (His) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cytochrome-c oxidase (BC 1.9.3.1) chain I - brine shrimp mitochondrion C; Species: mitochondrion Artemia franciscana (brine shrimp)
C; Date: 23 *Feb-1996 #sequence_revision 26-Jul-1996 #text_change 07-Dec-1999
C; Accession: S60622; S60638
R; Valverde, J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                         A;Introns: 20/3; 155/3; 220/3; 317/1; 369/1; 384/3
A;Note: T25B15.110
C;Superfamily: Arabidopsis thaliana hypothetical protein F24B22.230
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
69.2%; Score 36; DB 2; Length 412;
Best Local Similarity 75.0%; Pred. No. 39;
Matches 6; Conservative 1; Mismatches 1; Indels
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                                                                                                                                                 A, Experimental source: cultivar Columbia, BAC clone T25B15 C, Genetics:
A, Map position: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library, June 1994 A;Reference number: 860622 A;Accession: 860622
                                                       A,Molecule type: DNA
A,Residues: 1-412 <ALC>
A,Cross-references: EMBL:AL132972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 146-311 <PER>
A;Cross-references: EMBL:X69067
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Matches 6; Conservative
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A; Genetic code: SGC4
                  A;Status: preliminary
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hypothetical protein MJ0958 - Methanococcus jannaschii
C;Species: Methanococcus jannaschii
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R;Bult, C.J.; Woerbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; resich, C.J.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.A;Attle: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii A;Reference number: A64300; MUID:96337999; PMID:8688087
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Cidatesion: T0390
Richacesion: T0390
Rizhao, Y.; Kung, S.D.; Bottino, P.J.
submitted to the EMBL Data Library, July 1995
A)-Bescription: 4-Coumarate: CoA ligase genes in rice: divergent structure and differenti
A;Reference number: 214921
A;Accession: T03390
RiDobner, T.; Wolf, I.; Emrich, T.; Lipp, M.
Eur. J. Immunol. 22, 2795-2799, 1992
Affiltle. Differentiation-specific expression of a novel G protein-coupled receptor from A; Reference number: $26667; MUID:93049615; PMID:1425907
A; Accession: 926667
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A;Residues: 1-569 <ZHA>
A;Cross-references: EMBL:L43362; NID:g893293; PIDN:AAA69580.1; PID:g893294
C;Genetics:
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A;Molecule type: DNA
A;Residues: 1-372 < LODS>
A;Cross-references: EMBL:X68149; NID:g29459; PIDN:CAA48252.1; PID:g29460
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C,Superfamily: Methanococcus jannaschii hypothetical protein MJ0958
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Best Local Similarity 85.7%; Pred. No. 54;
Matches 6; Conservative 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross.references: GDB:136235; OMIM:601613
A;Map postition: 15q26.1-15q26.1
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein
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128 LHKVNFY 134
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A.Accession: A64555
                                                                                                                                                                                                                                                                                                                                                                                        queuine tRNM-ribosyltransferase - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
C;Species: Helicobacter pylori
C;Species: Helicobacter pylori
C;Avarietr; strain J99
C;Accession: C71952
C;A
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A,Reference number: A71800; MUID:99120557; PMID:9923682
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A,Residues: 1-371 cARN>
A,Cross-references: 18-71 (SB:AE001464; GB:AE001439; NID:g4154789; PIDN:AAD05847.1; PID:g415479
A;Experimental source: strain J99
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A,Residues: 1-371 <TOX-
A;Cross-references: GB.AE000547; GB:AE000511; NID:g2313377; PIDN:AAD07350.1; PID:g231337
C;Superfamily: queuine tRNA-ribosyltransferase
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G protein-coupled receptor BLR1 - human
G.Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jul-2000
C;Accession: $26667
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C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 29-Sep-1999
C;Accession: A64555
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    Mismatches

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A;Gene: tgt
C;Superfamily: queuine tRNA-ribosyltransferase
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Matches 5; Conservative
                               6; Conservative
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                                                                                                                     2 LHKVHFY 8
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                                    Matches
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A;Note: 4cl.2 C;Superfamily: 4-coumarate-CoA ligase; acetate-CoA ligase homology C;Keywords: acid-thiol ligase; coenzyme A; flavonoid biosynthesis F;89-562/Domain: acetate-CoA ligase homology <ACL>

0 0; Gaps Query Match 67.3%; Score 35; DB 2; Length 569; Best Local Similarity 100.0%; Pred. No. 83; Matches 6; Conservative 0; Mismatches 0; Indels

2 LHKVHF 7 |||||| 540 LHKVHF 545 QQ ò

Search completed: December 16, 2003, 14:19:14 Job time : 11.3333 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 16, 2003, 14:06:35; Search time 5.6667 Seconds (without alignments) 74.689 Million cell updates/sec

Title: US-09-870-089B-5 Perfect score: 52 Sequence: 1 FLHKVHFYV 9

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	O9xpn6 helonias bu	bacteriop					P16442 h histo-blo		Q9tkb8 kunzea eric				P32302 homo sapien			Q42982 oryza sativ			-	rattus		P37960 bacillus su	P28627 saccharomyc		Q9uuh4 schizosacch		P41023 bacillus me	4,		Q9mvd9 michelia al	9 arpophyll		Q9ghe5 zantedeschi
	MATK HELBU	YOSI_BPT4	MATK_TRILU	MATK TRIUN		L100_ADECC				COX1_ARTSF	TGT_HELPJ	TGT_HELPY	CCR5_HUMAN	Y958 METJA	MATK_ARUDI	4CL2_ORYSA	PTE1_HUMAN	TRMU_BUCBP	CCR5_MOUSE	CCR5_RAT	MATK_ACCAL	MRGA_BACSU	IMP1_YEAST	GIDB_STRMU	ER25_SCHPO	HFLC_TREPA	DCDA_BACMT	MATK_BRASC	MATK NUPVA	MATK MICAL	MATK ARPGI	MATK_NYMOD	MATK_ZANAE
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Score	40	37	37	37	37	37	36	36	36	36	35	35	35	35	35	32	34	34	34	34	34	33	33	33	33	33	33	33	33	33	33	33	33
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PRT; 181 AA.

RESULT 2 Y051_BPT4 ID Y051_BPT4 STANDARD; AC P39240; Q96215;

1 FLHKVHFYV 9 | | | :: | | | | | 247 FLERIHFYV 255

8 8

Ogghb2 phoenix dac Optnb1 convallatia Optnb1 convallatia O99mv7 mus musculu Q07868 bacillus su Q07866 chlamydia m O84250 chlamydia t Q18115 caenorhabdi Q89a41 buchnera ap P94525 bacillus su P39907 bacteroides Q9jva4 neisseria m					phyta; Tracheophyta; ales; Melanthiaceae;	, Kawano S.; Phylogenetic analyses of	t group 2. MAT	yright. It is produced through a collaboration of Bioinformatics and the EMBL outstation. Institute. There are no restrictions on its tions as long as its content is in no way is not removed. Usage by and for commercial agreement (see http://www.isb-sib.ch/announce/isb-sib.ch).	3F CRC64;	Length 515; 1; Indels 0; Gaps 0;
MATK_PHODC	ALIGNMENTS	PRT; 515 AA.	Created) Last sequence update) Last annotation update) urase).	ink).	<pre>Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Spermatophyta, Magnoliophyta, Liliopsida, Lilialee, Helonias. TOLITAXID=50364,</pre>	æ. H.	.ces."; in splicing INTRON MATUR	This SWISS-PROF entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Br the European Bioinformatics Institute. There are no restimes by Aon-profit institutions as long as its content modified and this statement is not removed. Usage by an entities a requires a license agreement (See http://www.isb-cor.gend an email to license@isb-sib.ch).	791.1;	%; Score 40; DB 1; %; Pred. No. 4.1; 2; Mismatches
63.5 63.5 63.5 63.5 63.5 63.5 63.5 63.5		STANDARD;	(Rel. 41, Create (Rel. 41, Last s (Rel. 41, Last a (Intron maturase)	ata (Swamp p	ridiplantae; ; Magnolioph :364;	I N.A. loo S., Uted stematics of	95.4 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	ry is instit ormati inst tateme licer	3AA36 42; 66; itron ttron chic	Similarity 66.7%; 6; Conservative
44449999944499999999999999999999999999		RESULT 1 MATK_HELBU ID MATK_HELBU AC 09XPN6:	2003 2003 2003 e K	MATK. Helonias bullata (Swamp pink) Chloroplast.	Eukaryota, Viridi Spermatophyta, Ma Helonias. NCBL TaxID=50364;	SEQUENCE FROM N.A. TISSUE-Leaf; Kazempour Osaloo S., Utech F.H., Ohara "Wolecular systematics of Trilliaceae	Trillium using J. Plant Res!- FUNCTION: - introns (B!- SIMILARITY SUBFAMILY.	This SWISS-PROF ent between the Swiss the European Bioinf was by Mon-profit modified and this sentitives requires a or send an email to	EMBL, AB017375; BAA1 InterPro; IPR000442, InterPro; IPR02866; Ffam; PF01349; Intr Pfam; PF01824; Mark mRNA processing; Chi SEQUENCE 515 AA;	Query Match Best Local Simil Matches 6; C
,		RESULT MATK HI ID M	TO 0 0	S 8 8	88888	R R R R F	##00000 ##00000	388888888	58888888 88888888888888888888888888888	O Be

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                      Maharia N., Marusich E., Djavakhishvili T., Neitzel J., Peterson S., Awaya M., Eidermiller J., Canada D., Tracy J., Gailbreath K., Paddison P., Anderson B., Stidham T., Blattner F., Kutter E.M., "The 10.7 kb' nonessential' region of bacteriophage T4 between the genes tk and nrdC: twenty new t4 genes, generally conserved among
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Liliales, Trilliaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kazengur Osaloo S., Utech F.H., Ohara M., Kawano S.,
"Molecular systematics of Trilliaceae I. Phylogenetic analyses of
Trillian using matK gene sequences.";
J. Plant Res. 112:35-49(1999).
-!- FUNCTION: Probably assists in splicing chloroplast group II
introns (By similarity).
-!- SIMILARITY: BELONGS TO THE INTRON MATURASE FAMILY 2. MATK
-!- SIMILARITY:
                                                                                                         Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
T4-like viruses.
01-FEB-1995 (Rel. 31, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
48-PEB-2003 (Rel. 41, Last annotation update)
Hypothetical 21.1 kDa protein in mobD-ri intergenic region.
YOSI OR MOBD.1 OR TK.-9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71.2%; Score 37; DB 1; Length 181; 83.3%; Pred. No. 5.1; Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                       Kutter E., Arieaka F., Kunisawa T., Tsugita A., Mosig G., Mesyanzhinov V., Ruger W., Stidham T., Thomas E.; Bacteriophage V. 14 genome analysis. J. Submitted (JUL-2000) to the BMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                      T-even phages,";
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
SEQUENCE 181 AA; 21177 WW; E51430751E2EAF3C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.SEP-2003 (Rel. 42, Created)
15.SEP-2003 (Rel. 42, Last sequence update)
15.SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Trillium luteum (Yellow wakerobin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U76612; AAB26969.1; -.
EMBL; AF158101; AAD42593.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Maturase K (Intron maturase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 83.3
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65 HKIHFY 70
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                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                     NCBI_TaxID=10665;
                                                                                               Bacteriophage T4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rissue=Leaf;
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                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chloroplast.
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Lilliopsida, Lilliales, Trilliaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kazempour Osaloo S., Utech F.H., Ohara M., Kawano S.; Molecular systematics of Trilliaceae I. Phylogenetic analyses of Trillium using matK gene sequences."; J. Plant Res. 112:35-49(1999).

-!- FUNCTION: Probably assists in splicing chloroplast group II introns (By similarity).

-!- SIMILARITY: BELONGS TO THE INTRON MATURASE FAMILY 2. MATK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 37; DB 1; Length 515;
Pred. No. 15;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                Pfam; PF01348; Intron_maturas2; 1.
Pfam; PF01824; MatK N; 1.
mRNA, processing; Chloroplast.
SEQUENCE 515 AA; 61074 MW; 6D750AF7P444DB50 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA processing; Chloroplast.
SEQUENCE 515 Aa; 61306 MW; 1CB6F63DFB45AED4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rrillium undulatum (Painted trillium).
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InterPro; IPR000442; Intron_maturse2.
InterPro; IPR002866; MatK N.
                                                                                                                                                           EMBL; AB017396; BAA36812.1; -.
InterPro; IPR000442; Intron_maturse2.
InterPro; IPR002866; MatK_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF01348; Intron_maturas2; 1. Pfam; PF01824; Matk N; 1.
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66.78;
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Best Local Similarity 66.73
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                  247 FLERTHFYV 255
                                                                                                                                                                                                                                                                                                                                                                               1 FLHKVHFYV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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Q9XPP8;
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Page 3

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BGAT HUMAN
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Spermatophyta, Magnoliophyta, Liliopsida, Liliales, Trilliaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kazempour Osaloo S., Utech F.H., Ohara M., Kawano S.; "Molecular systematics of Trilliaceae I. Phylogenetic analyses of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trillium using matK gene sequences.";
J. Plant Res. 112:35-49(1999).
-!- FUNCTION: Probably assists in splicing chloroplast group II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      introns (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF01148; Intronmaturas2; 1.
Pfam; PF011824; MatK N; 1.
mRNA processing; Chloroplast.
SEQUENCE 517 AA; 61378 MW; C18AB9643A7B5FED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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Canine adenovirus type 1 (strain CLL), and
Canine adenovirus type 1 (strain RI261).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trillium maculatum (Spotted wakerobin).
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InterPro; IPR000442; Intron maturse2.
InterPro; IPR002866; MatK_N.
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1 FLHKVHFYV 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=82490;
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J. Biol. Chem. 265:1146-1151(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
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                                                                                                                                                                    Morrison M.D., Onions D.E., Nicolson L., "Complete DNA sequence of canine adenovirus type 1."; J. Gen. Virol. 78:873-878(1997).
--i- FUNCTION: THE 100 kba PROTEIN IS A LATE NONSTRUCTURAL PROTEIN INVOLVED IN TRANSPORT OF HEXON FROM CYTOPLASM TO THE NUCLEUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Butheria, Primates, Catarihini, Hominidae, Homo.
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Yamamoto P.-I., Clausen H., White T., Marken J., Hakomori S.-I.;
"Molecular genetic basis of the histo-blood group ABO system.";
Nature 345:229-233(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P16442; 014490;
01-MUG-1990 (Rel. 15, Created)
01-DEC-1992 (Rel. 24, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
Histo-blood group ABO system transferase (NAGAT) [Includes:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71.2%; Score 37; DB 1; Length 689; 83.3%; Pred. No. 20; ative 1; Mismatches 0; Indels
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MEDLINE=90110099; PubMed=2104828;
Yamamoto F.-I., Marken J., Tsuji T., White T., Clausen H.,
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=95118355; PubMed=7598760;
                                                                                                                                         MEDLINE=97275900; PubMed=9129661;
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Pfam; PF02438; adeno 100; I.
Late protein; Transport.
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                                                                                                                                                                                                                                                                                                          Yamamoto F.1.; Hakomori S.1.;

"Sugar-uncleotide denor specificity of histo-blood group A and B
"Sugar-uncleotide denor specificity of histo-blood group A and B
"Lansferases is based on amino acid substitutions.";

"Biol. Chem. 265:19257-19262(1990).

"I show the histo-blood group ABO involves three carbohydrate antigens: A, B, and H. A, B, and AB individuals express a glycosyltransferase activity that converts the H antigen to the A antigen (by addition of UDP-GalMac) or to the B antigen (by addition of UDP-GalMac) or to the B antigen (by addition of UDP-GalMac) or to the B antigen (by addition of UDP-Gal).

"CATALYTIC ACTIVITY: UD-N-acetyl. D-galactosamine + glycoprotein-alpha-D-galactosaminyl-(1,3)-[alpha-L-fucosyl-(1,2)]-D-galactose.

"CATALYTIC ACTIVITY: UDP-galactose + alpha-L-fucosyl-(1,2)-D-galactose.

"CATALYTIC ACTIVITY: UDP-galactose + alpha-L-fucosyl-(1,2)-D-galactose.

"CATALYTIC ACTIVITY: UDP-galactose + alpha-L-fucosyl-(1,2)-D-galactose.

"CATALYTOR TOTYTY: UDP-galactose + alpha-L-fucosyl-(1,2)-D-galactose.
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GO:0030173; C:integral to Golgi membrane; NAS.
GO:0004381; F:glycoprotein-fucosylgalactoside alpha-galac. . .; NAS.
GO:0004380; F:glycoprotein-fucosylgalactoside alpha-N-ace. . .; NAS.
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POLYMORPHISM: THE SEQUENCE SHOWN IS THAT OF THE A TRANSFERASE.
P FORM DIFFERS BY A FEW RESIDUES SUBSTITUTIONS, THE O PHENOTYPE
RESULT OF A SINGLE BASE FRAMESHIFT DELETION IN THE N-TERMINAL
EXTREMITY OF THE GENE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- PATHWAY: Glycosylation.
-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND FORM IN TRANS CISTERNAE OF GOLGT. SOLUBLE FORM IN BODY FLUIDS.
-!- PIM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 6.
                     Geurts van Kessel A.;
"Genomic cloning of the human histo-blood group ABO locus.";
Blochem. Blopbys. Res. Commun. 206:318-325(1995).
                                                                                           MEDINE=95298046; PubMed=7779106;
Bennett E.P., Steffensen R., Clausen H., Weghuis D.O.,
Geutts van Kessel A.;
"Genomic cloning A.th human histo-blood group ABO locus.";
Biochem. Biophys. Res. Commun. 211:347-347(1995).
                                                                                                                                                                                                                       Xamamoto F.-1.;
"Human histo-blood group ABO gene locus alleles.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
Bennett E.P., Steffensen R., Clausen H., Weghuis D.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, X84746; CAA59233.1; -. EMBL; X84747; CAA59233.1; JOINED. EMBL; X84748; CAA59233.1; JOINED.
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BMBL; X84750; CAA59233.1; JOINED.
EMBL; X84751; CAA59233.1; JOINED.
EMBL; X84752; CAA59233.1; JOINED.
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EMBL; AF134413; AAD26573.1; -.
EMBL; AF134414; AAD26574.1; -.
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PDB; 1LZ1; 28-AUG-02.
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                                                                                    SEQUENCE FROM N.A.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Myrtales; Myrtaceae; Kunzea.
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                                                                                                                           FUCOSYLGLYCOPROTEIN ALPHA-N-ACETYLGALACTOSAMINYLTRANSFERASE, SOLUBLE
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                                                                                                                                                                                                         SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).
                                                                                                                                                                                                                                                LUMENAL, CATALYTIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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G -> S (IN GROUP B TRANSFERASE).
/FTId=VAR 003411.

I -> M (IN GROUP B TRANSFERASE;
IMPORTANT FOR THE SPECIFICITY).
/FTId=VAR 003412.
G -> A (IN GROUP B TRANSFERASE;
G -> A (IN GROUP B TRANSFERASE;
FUID=VAR 003413.
                    InterPro; IPR005076; Glyco trans_6.
Pfam, PR03414; Glyco transf_6.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal-anchor; Golgi stack; Polymorphism; Blood group antigen;
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/FTId=VAR 003409.
R -> G (IN GROUP B TRANSFERASE)
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Pred. No. 15;
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GO; GO:0006486; P:protein amino acid glycosylation; NAS
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                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL)
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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Similarity 71.4%;
5; Conservative 2
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O'Brien M.M., Quinn C.J., Wilson P.G.;
"Molecular systematics of the Leptospermum suballiance (Myrtaceae).";
Aust. J. Bot. 48:621-628(2000).
-!- FUNCTION: Probably assists in splicing chloroplast group II
introns (By similarity).
-!- SIMILARITY: BELONGS TO THE INTRON MATURASE FAMILY 2. MATK
                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                        69.2%; Score 36; DB 1; Length 505; 55.6%; Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69.2%; Score 36; DB 1; Length 505; 55.6%; Pred. No. 22; ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                      2; Indels
                                      EMBL, AF184723, AAF05930.1; -.
INLECPEO, IPRO00442; Intron matures2.
Interpro. IPR002866; Mark N.
Pfam; PF01348; Intron maturas2; 1.
Pfam; PF01348; Mark N; 1.
Pfam; PF01824; Mark N; 1.
SEQUENCE 505 AA; 60711 MW; 41B5EC246DC096A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ssing; Chloroplast.
505 AA; 60657 MW; 20D2B47963263B8D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 512 AA.
                                                                                                                                                                                                                                                                    2; Mismatches
  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, AF184724, AAF05931.2, -.
InterPro; IPR000442; Intron_maturse2.
InterPro; IPR002866, Mark_N.
Pfan, PF01348; Intron_maturas2; 1.
Pfan, PF01824; Mark_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maturase K (Intron maturase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kunzea ericoides (Kanuka).
                                                                                                                                                                                                     Query Match
Best Local Similarity 55.0.
There 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                             238 FFERIHFYV 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | ::||||
238 FFERIHFYV 246
                                                                                                                                                                                                                                                                                                               1 FLHKVHFYV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 FLHKVHFYV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=106044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA processing;
SEQUENCE 505 AJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
COX1 ARTSF
ID COX1 ARTSF
AC Q37705;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MATK KUNER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                              MATTOR MA
q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=94223692; PubMed=8169960;
Perez M.L., Valverde J.R., Batuecas B., Amat F., Marco R., Garesse R.;
Perez M.L., Valverde J.R., Batuecas B., Amat F., Marco R., Garesse R.;
Speciation in the Artemia genus: mitochondrial DNA analysis of
bisexual and parthenogenetic brine shrimps.";
J. Mol. Evol. 38:156-168(1994).
-!- FUNCTION: CYTOCHOME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
-!- FUNCTION: CYTOCHOME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. CO I IS THE
CATALYTIC SUBUNIT OF THE BIXZYME ELECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
AND HENDA A OF SUBUNIT I TO THE BIMETALLIC CENTER FORMED BY HEME A3
AND COPPER B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---- PATHWAY: Respiratory chain; terminal step.
--- SUGCELLOLAR LOCATION: INTEGRAL MENBRANE PROTEIN. MITOCHONDRIAL
INNER MEMBRANE. CONTAINS 12 POTENTIAL TRANSMEMBRANE DOMAINS.
--- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IRON (HEME A3 AXIAL LIGAND) (PROBABLE).
IRON (HEME A AXIAL LIGAND) (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1'-histidyl-3'-tyrosine (By similarity)
                                                                                                                                                                                                                           Bukaryota; Metazoa; Arthropoda; Crustacea; Branchiopoda; Anostraca;
Artemiidae; Artemia.
NCBI TaxID=6661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IRON (HEME A AXIAL LIGAND) (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Cytochrome o oxidase polypeptide I (EC 1.9.3.1).
COI OR CO-I.
Attemia ganfranciscana (Brine shrimp) (Artemia franciscana).
Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR01165; CYCOXIDASEI.
PROSITE; PS00077; COX1; 1.
Oxidoreductase; Heme; Copper; Mitochondrion; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69.2%; Score 36; DB 1; Length 512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4AA1E1BBE64913E3 CRC64;
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COPPER B (PROBABLE).
COPPER B (PROBABLE).
COPPER B (PROBABLE).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Respiratory chain; Inner membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56491 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X69067; CAA48806.1; -. PIR; $60622; S60622.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P00396; 20CC.
InterPro; IPR000883; COXI.
Pfam; PF00115; COXI; 1.
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376 3
238 2
512 AA;
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les 6; Conser'
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CROSSLNK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             METAL
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TGT_HELPJ
ID __TGT_H
AC __Q9ZMF
DT __16-OC
DT __16-OC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- ČOFACTOR: Binds 1 zinc ion per subunit (By similarity).
-!- SIMILARITY: BELONGS TO THE QUEUINE TRNA-RIBOSYLTRANSFERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: Exchanges the guanine residue with 7-aminomethyl-7-deazaguanine in tRNAS with GU(N) anticodons (tRNA-Asp, -Asn, -His and -Tyr). After this exchange, a cyclopentendiol moiety is attached to the 7-aminomethyl group of 7-deazaguanine, resulting in the hypermodified nucleoside queucaine (Q) (7-(((4,5-cis-dihydroxy-2-cyclopenten-1-yl)amino)methyl)-7-deazaguanosine) (By
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=99120557; PubMed=9923682;
Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
Smith D.R., Noonan B., Guldla B.C., deJonge B.L., Carmel G.,
Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
                                                                                                                                  Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATALYTIC ACTIVITY: tRNA guanine + queuine = tRNA queuine +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
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R PIR; C71952; C71952.

R HANAP; MF 00168; -; 1.

R InterPro; IPR004803; ORRNA_ribo_trans.

R InterPro; IPR004803; ORRNA_ribo_trans.

R Pfam; PF01702; 7GT; 1.

R TIGREAMS; TIGR0049; UG RNA_ribo_trans.

R TIGREAMS; TIGR0049; UG RNA_ribo_trans.

M CHANA processing; Zinc; Complete proteome.

M RACT_SITE 266 266 BY SIMILARITY.
28-FEB-2003 (Rel. 41, Last annotation update)
Queuine tRNA-ribosyltransferase (BC 2.4.2.29) (tRNA-guanine
transglycosylase) (Guanine insertion enzyme).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            155668901BB7FC3D CRC64;
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ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 35; DB Pred. No. 25;
                                                                                                                                                                                                 Helicobacteraceae; Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     266 266 BY
303 303 ZII
305 305 ZII
308 ZIII
334 334 ZIII
371 AA; 41506 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67.3%;
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es 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               333 LHNLHFYL 340
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                                                                                                                                                                                                                                      NCBI_TaxID=85963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similarity).
                                                                                                       JHP0266.
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                                                                                                                                                               STRAIN=26695 / ArCC 700392;
MREDLINE=9739467; PubMed=9252185;
Tomb U.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Tomb U.-F., White O., Kerlavage A.R., Klenk H.-P., Gill S., Dougherty B.A.,
Pleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,
Berg D.E., Goodayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
Cotton M.D., Weidman J.M., Pujil C., Bowman C., Watthey L., Wallin B.,
Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
-!- SIMILARITY: BELONGS TO THE QUEUINE TRNA-RIBOSYLTRANSFERASE FAMILY.
                                                                                   Bacteria; Profeobacteria; Epsilonprofeobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
                                                                                                                                                                                                                                                                                                                                              "The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- CATALYTIC ACTIVITY: tRNA guanine + queuine = tRNA queuine +
28-FEB-2003 (Rel. 41, Last annotation update)
Queuine tRNA-ribosyltransferase (EC 2.4.2.29) (LRNA-guanine
transglycosylase) (Guanine insertion enzyme).
TGT OR HP0281,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIGRFAMS; TIGRO0430; O tRNA tgt; 1.
TIGRFAMS; TIGRO0449; tgt gemeral; 1.
Queuosine biosynthesis; Transferase; Glycosyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
N -> KH (IN STRAIN P1).
N -> D (IN STRAIN P1).
A -> V (IN STRAIN P1).
E -> G (IN STRAIN P1).
E -> G (IN STRAIN P1).
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ACT SITE 91 91 BY SIMILARITY.
ACT SITE 266 266 BY SIMILARITY.
                                                                      Helicobacter pylori (Campylobacter pylori).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE000547; AAD07350.1; -.
EMBL; Y12061; CAA72784.1; -.
EMBL; Y2061; CAA72784.1; -.
EMBL; P28720; 1PUD.
TIGR; HP0281; -.
HAMAP; MF 00168; -; 1.
InterPro; IPR004803; QtRNA_ribo_trans.
InterPro; IPR002616; tRNA_ribo_trans.
Pfam; PF01702; TGT; 1.
                                                                                                                                                                                                                                                                                                                                                                              Nature 388:539-547(1997).
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                                                                                                                   NCBI TaxID=210;
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01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
C-X-C chemokine receptor type 5 (CXC-R5) (CXCR-5) (Burkitt'S lymphoma receptor 1) (Monocyte-derived receptor 15) (MDR15).
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-!- FUNCTION: CYTOKINE RECEPTOR THAT BINDS TO BLC. BIRI EXERTS POSSIBLY A REGULDATORY FUNCTION IN BURKITT LYMPHOMA (BL) LYMPHOMAGENESIS AND/OR B-CELL DIFFERENTIATION. IT IS A POTENTIAL CANDIDATE FOR CELL-CELL INTERACTION, AND ACTIVATION OF MATURE B-LYMPHOCYTES IN LYMPHOTIC TISSUES.

-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- ALTERNATIVE PRODUCTS:

EVENT.=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Legler D.F., Loetscher M., Stuber Roos R., Clark-Lewis I., Baggiolini M., Moser B., "Be cell-attracting chemokine I, a human CXC chemokine expressed in lymphoid tissues, selectively attracts B lymphocytes via
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Lymphocytes;

BIDLINE=93049615; PubMed=1425907;

Dobner T., Wolf Intich T., Lipp M.;

Differentiation-specific expression of a novel G protein-coupled receptor from Burkitt's lymphoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
G --> V (IN STRAIN P1).
Y --> Q (IN STRAIN P1).
Y --> G (IN STRAIN P1).
SK --> NN (IN STRAIN P1).
SK --> NN (IN STRAIN P1).
K --> N (IN STRAIN P1).
E --> K (IN STRAIN P1).
B --> K (IN STRAIN P1).
A --> T (IN STRAIN P1).
B --> K (IN STRAIN P1).
A --> T (IN STRAIN P1).
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                                                                                                                                                                                                                                                                                                                                                                                            67.3%; Score 35; 62.5%; Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eur. J. Immunol. 22:2795-2799(1992).
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                                                                                                                                                                                                                                                                                                                                          41415 MW;
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tes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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1177
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258
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371 AA;
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SEQUENCE
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                                                                                                                                                                                                                                                           MIM, 601613; -. Gintegral to plasma membrane, TAS. GO; GO:0005887. C:integral to plasma membrane, TAS. GO: 0016928; P:cell motility; TAS. GO; GO:0006928; P:cell motility; TAS. GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS. InterPro; IPR000276; GPCR_Rhodpsn.
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                              LYMPHOMA CELLS.
-:- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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PROSITE; PS00237; GPROTEIN RECEP F1 1; 1.
PROSITE; PS00237; G PROTEIN RECEP F1 2; 1.
G-protein coupled creeptor; Transmembrane; Glycoprotein; B-cell; Alternative splicing; Polymorphism.
1sold=P32302-2; Sequence=VSP 001892;
SGUE SPECIFICITY: EXPRESSION MATURE B-CELLS AND BURKITT
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/FTId=VSP 001892.
G -> S (IN dbSNP:665648).
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EXTRACELLULAR (POTENTIAL).
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Archaea; Euryarchaeota; Methanococci; Methanococales;
Methanocaldococcaceae; Methanocaldococcus.
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15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein MJ0958 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     426 AA.
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Genew; HGNC:1060; BLR1.
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145
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ses 6; Conserv
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TRANSMEM
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                                                                    MEDLINE=96337999; PubMed=868087;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., Fitzderald L.M., Clayton R.A., Gocayne J.D.,
Sutton G.G., Kirkness E.R., Tomb J.F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.M., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Rosales; Rosaceae; Rosaceae incertae sedis; Aruncus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- FUNCTION: Probably assists in splicing chloroplast group II introns (By similarity).
-i- SIMILARITY: BELONGS TO THE INTRON MATURASE FAMILY 2. MATK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Potter D., Gao F., Oh S.-H., Baggett S.; "Phylogenetic relationships among putative genes encoding polygalacturonase inhibitor proteins (PGIPs) in Rosaccae."; Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67.3%; Score 35; DB 1; Length 426; 57.1%; Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL PROTEIN MJ0958.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 426 AA; 50694 MW; 25317BE81E203A99 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein; Signal; Complete proteome. SIGNAL 1 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@igb-sib.ch).
                                         SEQUENCE FROM N.A.
STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aruncus dioicus (Goat's beard).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Maturase K (Intron maturase).
                                                                                                                                                                                                                                                                                                      Jamascn11.";
Science 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U67539; AAB98971.1; -.
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Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           426
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TIGR; MJ0958; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    358 HKLHYYI 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 HKVHFYV 9
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  NCBI_TaxID=2190;
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Q8WJR4;
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Q9cwl2 mus musculu 9vhm2 drosophila 960b2 drosophila

29bt16 homo sapien

homo sapien homo sapien pisolithus

Q8wx49 09x1p0

hygrophorop

siphonochil siphonochil campylobact

plasmodium plasmodium dendrophyla harrisella harrisella

dendrophyla trillium pe daiswa thib

caenorhabdi vibrio chol

09xlns | 08kwr | 08kwr | 08kwr | 08kwr | 08kwr | 08kwr | 08g | 08g | 08kwr | 0

trillium di paris thibe daiswa viol

Q9xpn8 Q9ghc4 Q9xr22

trillium pu trillium lu kinugasa ja

09xpp4 09xpp0 09xr21

09xr24 daiswa poly

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Nakagawa S.;
"Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
"Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AP005283; BAC00249.1; -.
Complete proteome; Hypothetical protein.
SEQUENCE 1043 AA; 112335 MW; 2A44C0E5431A29FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Corymebacterium glutamicum (Brevibacterium flavum).
Bayderia, Actinobacteria, Actinobacteridae; Actinomycetales;
Oorymebacterineae; Corynebacteriaceae; Corynebacterium.
WCBI_TaxID=1718;
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
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Last annotation update)
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STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
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01-MAR-2001 (TrEMBLrel. 16, Last seqn
01-0CT-2002 (TrEMBLrel. 22, Last ann
                 Q9CWL2
                                                      Q960B2
Q8WX49
Q9NXC6
Q9XLP0
Q9XLN5
Q9XKN1
                                                                                                                                                                              Q8HV19
Q8HV18
Q81389
Q81AY5
Q9GS12
Q8KQW4
Q8HRJ6
Q8HRJ6
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QBHRJ2
Q9XPP3
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les 7; Conservative
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Q9GHD1;
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QBNLT2
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Q9ghd5 heloniopsis
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                                                                                                                                       December 16, 2003, 14:09:45; Search time 25 Seconds (without alignments) 92.899 Million cell updates/sec
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09ghc6
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                 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                               830525 segs, 258052604 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                  OM protein - protein search, using sw model
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sp_virus:*
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Maximum DB seq length: 2000000000
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Match Length DB
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Best Local Similarity 66.7%; Pred. No. 24; Matches 6; Conservative 2; Mismatches
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247 FLERIHFYV 255
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                                                              1 FLHKVHFYV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-pink flower;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                  09GHC9;
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The plant biol 2:415-427(2000)

The plant biol 2:415-427(2000)

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Fuse S., Tamura M.N.;
Rup bylogenetic analysis of the plastid matk gene with emphasis on
Melanthiaceae sensu lato.";
Plant Biol. 2:415-4772000).
-!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
INTRONS (BY SIMILARITY).
-!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
--- AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
MITOCHONDRIAL INTRONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
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                                                                              Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Liliales, Melanthiaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76.9%; Score 40; DB 8; Length 515; 66.7%; Pred. No. 24; ive 2; Mismatches 1; Indels
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InterPro; IPR000442; Intron maturse2.
InterPro; IPR002866; Matk N.
Pfam; PF01348; Intron maturas2; 1.
Pfam; PF01824; Matk N.
Pfam; PF01824; Matk N.
Pfam; PF01824; Matk N.
Pfam; PF01824; Matk N.
SEQUENCE 515 AA; 61747 MW; 66A8A11DDA39BFBB CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Intron maturase (Maturase K).
  Intron maturase (Maturase K)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                          Heloniopsis orientalis.
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wes 6; Conserv
                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                             NCBI_TaxID=87628;
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                                                                                                                               Heloniopsis.
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Matches
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-!-SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED R
MITOCHONDRIAL INTRONS.
EMBL, AB040194; BAB16802.1; -.
INTEPPO; IPRO00442; INLTON maturse2.
InterPro; IPRO00442; INLTON maturse2.
Pfam; PP01348; Intron maturse2; 1.
Pfam; PP01348; Intron maturse2; 1.
Pfam; PP01348; Chloroplast.
SEQUENCE 515 AA; 61886 MW; 495CO6AD09F7FE66 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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"A phylogenetic analysis of the plastid matK gene with emphasis on Melanthiaceae sensu lato.",
Plant Biol. 2:415-427 (2000).
-i- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
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Fuse S., Tamura M.N.;
"A phylogenetic analysis of the plastid matK gene with emphasis on Melanthiaceae sensu lato.";
Plant Biol. 2:415-427(2000).
                                                                                                                                                                     Chloroplast.
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Melanthiaceae;
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Liliales, Melanthiaceae,
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                                       01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Intron maturase (Maturase K).
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515 AA
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us-09-870-089b-5.rspt

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Intron maturase (Maturase K)
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INTRONS (BY SIMILARITY)
-!- FINCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
INTRONS (BY SIMILARITY)
-!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
MITOCHONDRIAL INTRONS.
EMBL, AB040195; BABIESO3.1; -.
InterPro; IPRO0442; Intron_maturse2.
InterPro; IPRO0442; Intron_maturse2.
InterPro; IPRO0466; Matk.N.
Pfam; PF01148; Intron_maturas2; 1.
Pfam; PF01148; Intron_maturas2; 1.
SPGMF, Matk.N.; 1.
MRNA processing; Chloroplast.
SEQUENCE S15 AA; 61945 MW; BBSOEOAR2DBDIF88 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fuse S., Tamura M.N.;

Ruse S., Tamura M.N.;

"A phylogenetic analysis of the plastid matk gene with emphasis on melanthiaceae sensu late.";

Plant Biol. 2:415-427(2000).

-!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II

INTRONS (BY SIMILARITY).

-!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,

AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY MITOCHONDRIAL INTRONS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Melanthiaceae;
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                                                                                                                                                                                                                                                                                     Score 40; DB 8; Length 515; Pred, No. 24;
                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMEL, ABO40191; BAB16799.1; -
InterPro; IPR000442; Intron maturse2.
InterPro; IPR002866; Matk N.
Ffam; PP01348; Intron maturas2; 1.
Ffam; PP0424; Matk N; 1.
mRNA processing; ChIoroplast.
SEQUENCE 515 AA; 61780 MW; A4932FD7A8600BA8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                   2; Mismatches
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                                                                                                                                                                                                                                                                                          76.9%;
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Best Local Similarity 66...
Local 6; Conservative
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247 FLERIHFYV 255
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Q9GHC5;
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Q9GHC5
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Q9GHD2
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Plant Biol. 2:415-427(2000).
-!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
INTRONS (BY SIMILARITY).
-!- SIMILARITY WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
MITOCHONDRIAL INTRONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                    Fuse S., Tamura M.N.; m.A. phylogenetic analysis of the plastid matk gene with emphasis on Melathiaceae sensu latoo."; Plant Biol. 2:415-427(2000).
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Liliales, Melanthiaceae,
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                    Chloroplast.
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Liliales, Melanthiaceae,
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Pfam; PF01344; MatK N; 1.
BRNA, processing; Chloroplast.
SEQUENCE 515 AA; 61919 MW; 556C6A17A69204FF CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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InterPro; IPR000442; Intron maturse2.
InterPro; IPR002866; MatK N.
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nes 6; Conservative
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Chionographis japonica.
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Fuse S., Tamura M.N.;
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Gaps

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INTRONS (BY SIMILARITY).

-!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
MITOCHOUDRIAL INTRONS.

EMBL, ABG40189; BAB16797.1; -
InterPro; IPR000442; Intron maturse2.
InterPro; IPR000442; Intron maturse2.
Feam; PF01348; Intron maturse2; 1.
Pfam; PF01348; Intron maturse2; 1.
RFMA processing; Chloroplast.
SEQUENCE 515 AA; 61916 MW; 7EB6D08388182890 CRC64;
INTRONS (BY SIMILARITY).
-!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
MITOCHONDRIAL INTRONS.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Melanthiaceae;
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Plant Biol. 2:415-427(2000).
-!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
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                                                                                                                                                                                                                                                                                                                                                           76.9%; Score 40; DB 8; Length 515; 66.7%; Pred. No. 24; 1; Indels rative 1; Assmatches 1; Indels
                                                                                                                         EMBL, AB040193; BAB16801.1; -.
InterPro; IPR000442; Intron maturse2.
InterPro; IPR002666; Mark N.
Pfam; PF01348; Intron maturas2; 1.
Pfam; PF01844; Mark N; 1.
mRNA processing; Chloroplast
SEQUENCE 515 AA; 61844 MW; 1BBFF413F5DE7848 CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Intron maturase (Maturase K)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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Matches 6; Conservative
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247 FLERIHFYV 255
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                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
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Fuse S., Tamura M.N.;
Fuse S., Tamura M.N.;
A phylogenetic analysis of the plastid matK gene with emphasis on Melanthiaceae sensu lato.";
Plant Biol. 2:415-427(2000).
-!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chloroplast.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Melanthiaceae;
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Spermatophyta, Magnoliophyta, Liliopsida, Liliales, Melanthiaceae,
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            1; Indels
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Intron maturase (Maturase K).
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les 6; Conservative
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               6; Conservative
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Fuse S., Tamura M.N.;
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01-OCT-2002
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"A phylogenetic analysis of the plastid matk gene with emphasis on melanthiaceae sensu lato.";
Melanthiaceae sensu lato.";
Plant Biol. 2:415-427(1200);
-:- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II INTRONS (BR SIMILARITY).
-:- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
                                                                                                                            Fuse S., Tamura M.N.;

Ruse S., Tamura M.N.;

"A phylogenetic analysis of the plastid matk gene with emphasis on melanthiaceae sensu lato.";

Plant Biol. 2:415-427(2000).

-!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II

INTRONS (BY SIMILARITY).

-!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,

AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY MITOCHONDRIAL INTRONS.
                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
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Spermatophyta, Magnoliophyta, Liliopsida, Liliales, Melanthiaceae,
                                 Chloroplast.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Melanthiaceae;
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Pfam; PF01344; MatK N; 1.
RNA processing; Chloroplast.
SEQUENCE 515 AA; 61796 MW; ICBFFF71CAF6CEF8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MRNA processing; Chloroplast.
SEQUENCE 515 AA; 61926 MW; FB689B0255959075 CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Intron maturase (Maturase K).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   515 AA
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InterPro; IPR000442; Intron maturse2.
InterPro; IPR002866; MatK_N.
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Matches 6; Conservative
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Best Local Similarity 66.77
Matches 6; Conservative
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                    rpsilandra thibetica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heloniopsis kawanoi.
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                                                                                       NCBI_TaxID=120020;
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SEQUENCE FROM N.A.
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PROTECTION OF THE PROM N.A.

PRUSE S., Tamura M.N.;

PRUSE S., Tamura M.N.;

PRUSE S., Tamura M.N.;

Melanthiaceae sensu lato.";

Plant Biol, 2:415-477(2000).

I. Plant Biol, 2:415-477(2000).

I. PUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II

INTRONS (BY SIMILARITY).

INTRONS (BY SIMILARITY).

INTRONS (BY SIMILARITY).

AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY MITOCHONDRIAL INTRONS.

RICHEPRO: IPRO00442; Introm matures2.

REMEL; AB40196; BAB16804.1; -.

RICHEPRO: IPRO02866; Matk N. N.

Péam; PF01348; Introm maturas2; 1.

Pfam; PF01348; Introm maturas2; 1.

REMEN; PROBERY N. Matk N. N.

Pfam; PROBABLY MATK N. N.

PFam; PROBABLY MATK N. N.

RICHEPRO: IPRO02866; Matk N. N.

PFam; PROBABLY MATK N. N.

PFAM; PROBABLY MATK N. N.

RICHEPRO: IPRO02866; MATK N. N.

PFAM; PROBABLY MATK N. N.

RICHEPRO: IPRO02866; MATK N. N.

PFAM; PROBABLY MATK N. N.

PFAM; PROBABLY MATK N. N.

RICHEPRO: IPRO02866; MATK N. N.

RICHEPRO: IPRO02866; MATK N. N.

PFAM; PROBABLY N. N. N.

RICHEPRO: IPRO02866; MATK N. N.

PFAM; PROBABLY N. N. N.

RICHEPRO: IPRO02866; MATK N. N.

PFAM; PROBABLY N. N. N.

RICHEPRO: IPRO02866; MATK N. N.

PROBQUENCE 515 AA; 61365 MW; DC2AC5306073DD09 CRC64;
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta; Liliopsida, Zingiberales, Zingiberaceae,
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Kress W.J., Prince L.M., Williams K.J.;
"The phylogeny and a new classification of the gingers (Zingibersecae): Evidence from molecular data.";
Am. J. Bot. 89:1684-1698(2002).
EMBL, AF478878; AAN63235.1; -.
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(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 22, Last annotation update)
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Last annotation update)
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01-MAR-2003 (TrEMBLrel. 23, Last sequ
01-MAR-2003 (TrEMBLrel. 23, Last anno
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Matches 6; Conservative
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247 FLERIHFYV 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=112831;
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SEQUENCE 5
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Query Match 76.9%; Score 40; DB 8; Length 515; Best Local Similarity 66.7%; Pred. No. 24; Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0; Qy 1 FLHKUHFYV 9

Db 247 FLERIHFYV 255
Search completed: December 16, 2003, 14:17:59
Job time: 27 secs
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Polyglutamine-glut Human ORFX protein Human immune/haema

Arabidopsis thalia Arabidopsis thalia

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Human peptidase-li

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immunogenic ligand, gene therapy; MHC; major histocompatibility complex;
adoptive immunotherapy; cancer, ovarian cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human cancer antigen ATP4/CREB-2 based immunogenic ligand #3.
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AAG76780
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ABG03108
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AAB46370
                                                   ABG00522
                                                                                          ABG30742
                                                                                                     AAE12188
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                                                                                                                                            AAG19315
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31-MAY-2000; 2000US-209388P.
20-DEC-2000; 2000US-257007P.
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WO200192306-A2,
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AAU74683
 Human cancer antig
Human cancer antig
Novel human diagno
Simian immunodeffi
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Drosophila melanog
Drosophila melanog
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Prophenol oxidase.
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                                                                                      ; Search time 33 Seconds (without alignments) 43.289 Million cell updates/sec
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| SIDSIJgcgdata/geneseqp.embl/AA1980.DAT:*
| SIDSIJgcgdata/geneseqp.embl/AA1981.DAT:*
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| SIDSIJgcgdata/geneseqg.embl/AA1981.DAT:*
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| SIDSIJgcgdata/geneseqg.embl/AA1991.DAT:*
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| SIDSIJgcgdata/geneseqg/genesegg-embl/AA1991.DAT:*
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                                                                                                                                                                                                                                                           1107863
            GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                   1107863 seqs, 158726573 residues
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                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                          December 16, 2003, 14:06:05
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ABG19706
AAR10276
AAW56104
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ABB57998
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AAW14441
                                                               OM protein - protein search, using sw model
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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Novel human secret Novel human diagno

Novel human diagno

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us-09-870-089b-7.rag

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The invention relates to compounds comprising an immunogenic ligand whose sequence is based in part on residues 42-50 of human cancer antigen ATF4(TERB-2 (Inct defined) and the polynucleotides encoding them. Also included are an antibody that specifically recognises and binds the compound, a method for inducing an immune response in a subject by delivering the compound, a method of immunotherapy comprising deministering to a subject the antibody, an immune effector cell that has been raised in vitro or in vivo in the presence and at the expense of an intigor presenting cell that presents the immunogenic compound in the context of an MHC (major histocompatibility complex) molecule and a method of adoptive immunotherapy comprising administering the immune response to the synthetic and naturally occurring compounds. The compounds are useful for modulating an immune response to the synthetic and naturally occurring compounds. The compounds are useful for generating antibodies for compounds are useful for generating antibodies continued are also useful for generating antibodies that specifically recognise and bind to these molecules. These compounds are useful for immunotherapy when administered to a subject. The peptides, polypeptides and polynucleotides are useful in diagnostic methods, for the detection and purification of antibodies. The sequence represents a human cancer antigen ATP4/CRBB-2 based immunogenic contraction of the invention invention and purification of antibodies. The present invention in an alman cancer antigen ATP4/CRBB-2 based immunogenic contraction of the invention in an antipodies. The present antigen and purification of antibodies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, cancer antigen, ATF4; CREB-2; vaccine; cytostatic; immunogenic ligand; gene therapy, MHC; major histocompatibility complex; adoptive immunotherapy; cancer; ovarian cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   respectively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: Immunogenic ligands AAU74681-AAU74686 are stated to be encoded by the degenerate DNA sequences AAS20120-AAS20125 respective) but have not been cross-referenced or CDS features put in due to the degeneracy of the DNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
New therapeutic compounds comprising immunogenic ligands, useful for modulating an immune response, particularly for treating ovarian cancer, and as components of anticancer vaccines -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human cancer antigen ATF4/CREB-2 based immunogenic ligand #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 61; DB 23; Length 9; 100.0%; Pred. No. 9.3e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU74684 standard; Peptide; 9 AA.
                                                                                          Claim 3; Page 55; 68pp; English.
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20-DEC-2000; 2000US-257007P.
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The invention relates to compounds comprising an immunogenic ligand whose sequence is based in part on residues 42-50 of human cancer antigen ATF4(TREB-2 (Inct defined) and the polymucleotides encoding them. Also included are an antibody that specifically recognises and binds the compound, a method of immunotherapy comprising the delivering the compound, a method of immunotherapy comprising been raised in vitro or in vivo in the presence and at the expense of an antigen presenting cell that presents the immunogenic compound in the context of an MHC (major histocompatibility complex) molecule and a method of adoptive immunotherapy comprising administering the immune response context of an MHC (major histocompatibility complex) molecule and a method of adoptive immunotherapy comprising administering the immune response to the synthetic and naturally occurring compounds. The compounds are useful for modulating an immune response to the synthetic and naturally occurring compounds. The compounds are useful for treating cancer, particularly ovarines. The compounds are also useful for generating antibodies that specifically recognise and bind to these molecules. These antibodies are large are also useful for generating antibodies con as immunogens for the detection and purification of antibodies, or as immunogens for the production of antibodies. The persent and purpaid and purpaid antibodies. The present immunoter represents a human cancer antigen ATF4(RRB-2 based immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Note: Immunogenic ligands AAU74681-AAU74686 are stated to be encoded by the degenerate DNA sequences AAS20120-AAS20125 respectively but have not been cross-referenced or CDS features put in due to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                  useful for
                                                                              New therapeutic compounds comprising immunogenic ligands, useful modulating an immune response, particularly for treating ovarian cancer, and as components of anticancer vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      degeneracy of the DNA sequences.
                                                                                                                                                                        Claim 4; Page 56; 68pp; English.
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                                       WPI; 2002-097764/13.
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Nicolette CA;
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lacking the vpx gene).
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                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                172 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference 11
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                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                         AAWS6104;
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                                                                                                                                                                                                                                                  음
                                                                                                                                                                  The invention relates to isolated polynuclectide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (FCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynuclectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in alectronic format directly from WIPO at ftp. wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78.7%; Score 48; DB 22; Length 1248; 75.0%; Pred. No. 78; 0; Indels cive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Simian immunodefficeincy virus vif protein.
                                                                                                                                                Claim 20; SEQ ID No 50065; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIVmnd; HIV; AIDS; vaccine; pSMH103.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR10276 standard; Protein; 172 AA.
                         Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Simian imunodeficiency virus.
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nes 6; Conservative
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                        Drmanac RT, Liu C,
                                                WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1248 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TOFU ) TONEN CORP.
(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAQ10203.
                                                               N-PSDB; AAS83893
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR10276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                        a vaccine
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                         SIV proteins may be produced from an E.coli expression system transformed with plasmid pSMH103.
These may be used in diagnosis, treatment, and development of a vacagainst AIDS, as the sequence has the same structure as HIV-1 (but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, telomerase reverse transcriptase, hTRT, TRT, diagnosis, prognosis, cell proliferation, cancer, ageing, ribonucleoprotein.
New complementary DNA to RNA gene of simian immuno-deficiency virus - used for preparing vaccine and diagnosis agent for AIDS
                                                                                                                                                                                                                                                                                                                                                                                                        .,
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                                                                                                                                                                                                                                                                                                                                              68.9%; Score 42; DB 12; Length 172; 62.5%; Pred. No. 84; 1; Indels ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  label= stop_codon
note= "encoded by TAA"
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note= "encoded by TAG"
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note= "encoded by TAG"
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note= "encoded by TGA"
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note= "encoded by TGA"
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'note= "encoded by TAG"
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/note= "encoded by TGA"
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'note= "encoded by TAA"
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/note= "encoded by TAA"
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'note= "encoded by TAG"
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/note= "encoded by TAG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW56104 standard; Protein; 587 AA.
                                                                             Claim 2; Fig 4; 14pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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TAA"	TGA" TAA"	TAA"	TGA"	TGA"	TAA"	TGA"	TAA"	TGA"	TGA"	TGA"	TGA"	TGA"	TAA"	TGA"	TGA"	TGA"	TAG"	TAG"	TAA "	TAG"	TAG"	TGA"	
el= stop e= "enco el= stop	coded coded	/label= stop_codon /note= "encoded by 155	/label= stop_codon /note= "encoded by	213 /label= stop_codon /note= "encoded by	218 /label= stop_codon /note= "encoded by	221 /label= stop_codon /note= "encoded by	233 /label= stop_codon /note= "encoded by	= stop_cod "encoded	45 label= stop_cod note= "encoded	281 /label= stop_codon /note= "encoded by	298 /label= stop_codon /note= "encoded by	/label= stop_codon /note= "encoded by	380 /label= stop_codon /note= "encoded by	/label= stop_codon /note= "encoded by	431 /label= stop_codon								
Misc-difference	Misc-difference	sc-differen	000000000000000000000000000000000000000)		מביים די ביים ביים	sc-dif	sc-di	Misc-difference	Misc-difference	Misc-difference	SC	sc-difference	sc-differenc	sc-dliterenc	c-differen		- ·-		sc-differenc		Misc-difference
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	Lingner J;
TAA" TAA" TAA" TAA" TAA" TAA" TAA" TAA" TAA"	TGA"
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sc-dif sc-dif sc-dif sc-dif sc-dif sc-dif sc-dif sc-dif	Misc-difference GB2317891-A. 08-APR-1998. 01-OCT-1997; 14-AUG-1997; 18-APR-1997; 25-APR-1997; 25-APR-1997; 19-MAY-1997; 14-AUG-1997; 14
	T T T T X X X X X Y X X X X X X X X X X

207 LHHWHW 212

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RESULT 7

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher enkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
                                                                                                                         Gaps
    its
                                                                                                                                                                                                                                                                                                                                                                            Drosophila; developmental biology; cell signalling; insecticide;
Pure and recombinant human Telomerase Reverse Transcriptase and variants - are useful in the diagnosis, prognosis and treatment cell proliferation conditions especially cancer and ageing
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                                                                                          Score 42; DB 19; Length 587;
Pred. No. 2.7e+02;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster polypeptide SEQ ID NO 5304.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Myers EW;
                                                                                                                                                                                                                                                           ABB59504 standard; Protein; 683 AA.
                                                                Example 1; Fig 35; 387pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Li PWD,
                                                                                             68.9%;
55.6%;
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11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid
genes from Drosophila and
interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 85...
                                                                                                                                                                                                                                                                                                                          26-MAR-2002 (first entry)
                                                                                                                         5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ABB57737-ABB72072).
                                                                                                                                                                                     FPHKWRWIL 33
                                                                                                                                                         FLHKWHWVV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PEKE ) PE CORP NY.
                                                                                       Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         683 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; ABL03607
                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                     pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-SEP-2001.
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                                                                                                                                                                                                                                                                                            ABB59504;
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                                                                                                                                                                                        25
                                                                                                                                                                                                                                                RESULT 6
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher wetkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                 Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 684;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67.2%; Score 41; DB 22; L
83.3%; Pred. No. 4.3e+02;
iive 0; Mismatches 1;
                                                                                       Drosophila melanogaster polypeptide SEQ ID NO 786.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (pro)phenoloxidase Phe52-Gly685.
                                                                                                                                                                                                                                                                                                                                           Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR89115 standard; Protein; 685 AA.
          ABB57998 standard; Protein; 684 AA
                                                                                                                                                                                                                                                                                                                                           Li PWD,
                                                                                                                                                                                                                                                                       23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                             23-MAR-2001; 2001WO-US09231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                               Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                           Adams M,
                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-656860/75.
N-PSDB; ABL02101.
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les 5, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequences (ABL0184(
(ABB57737-ABB72072)
                                                                                                                                                                                                                                                                                                               (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 LHKWHW 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               684 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                         interactions -
                                                                                                                                  pharmaceutical
                                                                                                                                                                                        WO200171042-A2
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                                                                 26-MAR-2002
                                                                                                                                                                                                                    27-SEP-2001
                                                                                                                                                                                                                                                                                                                                            Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                      ABB57998;
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Matches
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ABB57998
                         XXXXXXXXX
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Gaps

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67.2%; Score 41; DB 22; Length 683; 83.3%; Pred. No. 4.3e+02; ive 0; Mismatches 1; Indels

2 LHKWHW 7

95JP-0177444.

13-JUL-1995;

Peptide Peptide Peptide

Peptide

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The phenol oxidase may be used as a novel labelling oxidase. The elucidation of the primary structure of the prophenol oxidase will contribute to the reconstitution of a prophenol oxidase activation system which can be applied to the detection of microorganisms by measurement of beta-1,3-glucan and peptide glycan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
                                                                                                                                                                                                                                This protein is a prophenol oxidase derived from a domestic silkworm.
                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                   (Pro)phenol oxidase derived from a domestic silkworm - useful as a labelling oxidase and in pro-phenol oxidase activation system for detection of microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; colon cancer; colon cancer antigen; diagnosis; detection;
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                                                                                                                                                                                                                                                                                                                                                                          Score 41; DB 18; Length 685;
Pred. No. 4.3e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human colon cancer antigen protein SEQ ID NO:4964.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 11; Page 6720; 9803pp; English.
                                                                                                                                                                                                     Claim 2; Page 14-17; 18pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAG74200 standard; Protein; 41 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Birse CE,
                                                           LTD.
                                                                                                                                                                                                                                                                                                                                                                                 67.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-SEP-2000; 2000WO-US26524.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-SEP-1999; 99US-0157137.
03-NOV-1999; 99US-0163280.
                            95JP-0177444.
                                                           (WAKP ) WAKO PURE CHEM IND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      colorectal carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-235357/24.
                                                                                         WPI; 1997-148588/14.
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                                                                                                             N-PSDB; AAT62660.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                             13-JUL-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG74200;
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                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The B. mori silkworm larvae derived (pro)phenoloxidases Phe52-Val693 (AAR89114) and Phe52-Gly685 (AAR89115), are encoded by AAT10240 and AAT10241, respectively. The (pro)phenoloxidases can be used as new labelling oxidases.
                                                                                                                                                                                                                                                                                                                                                                                                                                              (Pro) phenol:oxidase from silkworm - useful as a labelling oxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              oxidase; prophenol; phenol; domestic silkworm; label; detection.
Silkworm; larvae; pro; phenoloxidase; Phe52-Val693; Phe52-Gly685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67.2%; Score 41; DB 17; Length 685; 83.3%; Pred. No. 4.3e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                               41..51
/note= "peptide fragment"
52..61
/note= "peptide fragment"
                                                                                                                                             "peptide fragment"
                                                                                                                 "peptide fragment"
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/note= "claim 1"
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/label= pro-sequence
53..685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2; Pages 14-17; 29pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW14441 standard; Protein; 685 AA.
                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                       (WAKP ) WAKO PURE CHEM IND LTD
                                                                                                                                                                                                                                                                                                           94JP-0085096.
                                                                                                                                                                                                                                                                                                                                            94JP-0085096
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                                                                                                                       'note=
                                                                                                                                                    'note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 685 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prophenol oxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 LHKWHW 7
                        labelling oxidase
                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAR89115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JP09023886-A.
                                                                                                                                                                                                                                               JP07289251-A
                                                                                                                                                                                                                                                                                                             22-APR-1994;
                                                                                                                                                                                                                                                                                                                                            22-APR-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bombyx mori
                                                                                                                                                                                                                                                                               07-NOV-1995
                                                          Bombyx mori
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Sequence

Matches

g ð

AAW14441;

Protein Peptide

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therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing c inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated PS, by inserting the nucleic acids into a host cell and culturing the cell compares the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB37789 represent sequences used in the exemplification of the present invention.

N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppessant; cardiant; immunostimulant; chrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiamatory; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel nucleic acids and peptides derived from open reading frame X,
                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                  DB 22; Length 41; 42;
                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human ORFX ORF688 polypeptide sequence SEQ ID NO:1376.
                                                                                                                                                                                                                                                                                                                                    Score 40; DB
Pred. No. 42;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB40924 standard; Protein; 59 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-1999; 99US-0127607.
02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
                                                                                                                                                                                                                                                                                                                                      65.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-MAR-2000; 2000WO-US08621.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 5v...
4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          thrombosis; contraceptive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leach M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-602362/57.
                                                                                                                                                                                                                                                                                                                                                                                                                                   27 LHPWNWII 34
                                                                                                                                                                                                                                                                                                                                                                                                             2 LHKWHWVV 9
                                                                                                                                                                                                                                                                                                    41 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAC75133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200058473-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  domo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB40924;
                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
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which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; sequences have activities such as: cytostatic; hepatotropic; vulnerary; antiparkinsonian; nootropic; neuroprotective; cartiparkinsonian; nootropic; immunosuppressant; cimmunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antichart; antiparkinal immunosuppressant; cimmunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; cartifilammatory; antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating cut perbological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy. Vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, cycliferative disorders, cardiavascular disease, diabetes mellitus, chopsthyroidism, cholesterol ester storage, systemic lupus cythematosus, severe combined immunodeficiency (SCID), AIDS, viral, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, cocurnal haemoglobinuria, antiinflammatory disease; to enhance constrund the construction; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; ORF; open reading frame; ORFX; drug screening; diagnosis; disease monitoring; cytokine; cell proliferation; cell differentiation; dimune modulation; haematopoiesis regulation; tissue growth; angiogenesis; activin; inhibin; chemotactic; chemokinetic; haemostatic; thrombolytic; tumour inhibition; bodily characteristic; fertility; behaviour; cancer; proliferative disorder; neurological disorder; cardiovascular disease; immune system disorder; organ transplantation; tissue growth disorder; tissue regeneration disorder; diabetes mellitus; hypothyroidism; cholesterol ester storage disease; infection; vulnerary; vasotropic; antipsoriatic; antidiabetic; cytostatic; nootropic; orandiatherosclerotic; anticoagulant; thrombolytic; cardiant; hypotensive; antistherosclerotic; antidiamatory; immunomodulator; dermatological; analgesic; virucide; antibacterial; fungicide.
                                                                                                                     AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65.6%; Score 40; DB 21; Length 59;
83.3%; Pred. No. 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human peptidase-like ORF54 protein, SEQ ID NO:108.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                         Claim 11; Page 1172; 5507pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABP31081 standard; 'Protein; 59 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-MAY-2001; 2001WO-US17076.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 83...
France 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19 LHGWHW 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 LHKWHW 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200190366-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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99WO-CA00272. 98US-0053197. 98US-0085761.

Turner RJ;

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Membrane targeting protein; translocation protein; Escherichia coli;
Sec-independent pathway; protein transport; twin-arginine signal peptide;
mttABC operon; MttA protein.
                                                                                                                                                                                                                                                                                                                         AAY41219 standard; Protein; 88 AA.
                                                                                                                                                                                                                                                                                                                                                        M. leprae YY34-MYCLE protein
                                                                                                                                                                                                                                                                                                                                             31-JAN-2000 (first entry)
                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 83.3;
5; Conservative
                WPI; 2002-106200/14
                                                                                                                                                                                                                                                                                              LHGWHW 24
                                                                                                                                                                                                                                                                                    2 LHKWHW 7
                                                                                                                                                                                                                                                      59 AA;
                     N-PSDB; ABN75107
                                               transplantation
                                                                                                                                                                                                                                                                                                                                   AAY41219;
      Leach MD,
                                                                                                                                                                                                                                                                                               19
                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                               RESULT 13
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The invention relates to recombinant membrane targeting and translocation proteins from Escherichia coli. The recombinant pathway for transporting polypeptides are involved in the Sec-independent pathway for transporting proteins with a twin- arginine signal peptide to the periplasm or extracellular medium and to the cell membrane. They transport fully catracellular medium and to the cell membrane. They transport fully colded and co-factor containing proteins. The polypeptides are used to transport such proteins, specifically to produce soluble forms of polypeptides that are normally produced in insoluble form. They may also be used to raise specific antibodies. Nucleic acid sequences that encode the polypeptides are used for production of recombinant proteins and their fragments are used as probes to detect or isolate related genomic or cDNA sequences (these have been found in many other bacteria, yeast, plants, nematodes and humans). Producing normally insoluble proteins in denaturants and facilitates recovery of functional proteins (which have been properly folded by cytoplasmic enzymes before translocation).

Sequences AAV41214-41223 represent proteins homologous to the E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New recombinant membrane targeting and translocation proteins from Escherichia coli, used to produce soluble polypeptides normally produced in insoluble form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 6; Fig 8; 111pp; English.
   Mycobacterium leprae.
                                                                                                                                                                                                                                                                                                                                                                (UYAL-) UNIV ALBERTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-633740/54.
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                                                                                                                                                                                                   29-MAR-1999;
                                                                                                                                                                                                                                                                 01-APR-1998;
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                                                                 W09951753-A1
                                                                                                                                  14-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                              Weiner JH,
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ð
                                                                                                                                                                                                                                                                                                                                                                                                                                            C designated ORF (open reading frame) 1-4534, and sequences ABM7504-
ABM79587 represent cDNAs encoding them. The invention also encompasses
C ABM79587 represent cDNAs encoding them. The invention also encompasses
polyapeptides at least 80% identical to the ORF1-ORF434 (collectively
referred to as ORFX) proteins, polymucleotides at least 85% identical to
creferred to as ORFX proteins, methods and host cells comprising ORFX
polyupeptides, methods of screening for modulators of ORFX proteins antibodies
CC specific for ORFX proteins, methods of derecting ORFX proteins and methods of screening individuals for a predisposition or
activity, and methods of screening individuals for a predisposition or
activity, and methods of screening individuals for a predisposition or
activity, and methods of acreening individuals for a predisposition or
compared a disorder. The ORFX proteins of the invention have a wide
creaptor/ligand, antibities, such as cytokine, cell proliferation,
call differentiation, immune modulation, haematopoiesis regulation,
cell differentiation, antibities, such as cytokine, cell proliferation,
conflexible growth, anglogenesis, activin or inhibin activity, chemotactic/
chemokinheit activity, and may also be involved in the determination
conflexible and antibodies may be used in the treatment of cancers,
conclete acids and antibodies may be used in the treatment of cancers,
conterporiferative disorders such as spoilapsy and Alzheimer's disease,
conterpolated disorders such as goliapsy and Alzheimer's disease,
conterpolated disorders such as goliapsy and Alzheimer's disease,
content proliferative and probes, in the detection of ORFX genomic sequences,
contents and infectious diseases caused by viral, bacterial
contents and and antipolate mell
                                                                                                                                                                                            Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and disorders related to organ
                                                                                                                                                                                                                                                                                                                                                                                                                                  ABP31028-ABP35561 represent 4534 novel human proteins
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                                                                                                                                                                                                                                                                                                                                                                       Claim 10; Page 297; 2508pp; English.
                                            Shimkets RA;
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ö Gaps Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder. .. 0 Score 40; DB 20; Length 88; Pred. No. 86; 0; Mismatches 2; Indels Novel human diagnostic protein #513. ABG00522 standard; Protein; 123 AA. Match 65.6%; Local Similarity 75.0%; hes 6; Conservative 6 (first entry) 4 LSPWHWVV 11 2 LHKWHWVV 9 88 AA; WO200175067-A2 13-FBB-2002 Homo sapiens 11-OCT-2001. ABG00522; RESULT 14 ABG00523 a EXEXEX SX EXEX EX EX SX EX SX

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Gaps

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30-MAR-2001; 2001WO-US08631.

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990S-0139452.
990S-0139493.
990S-0139492.
990S-0139454.
990S-0139455.
990S-0139456.
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99US-0140695.
99US-0140823.
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99US-0139462.
99US-0139463.
99US-0139750.
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99US-0139817.
99US-0139899.
99US-0140353.
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99US-0141287.
99US-0141842.
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990S-0134218.
990S-0134219.
990S-0134221.
99US-0134370.
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99US-0135124.
99US-0135353.
99US-0135629.
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99US-0136782.
99US-0137222.
99US-0137528.
99US-0137528.
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99US-0138847.
99US-0139119.
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99US-0132486.
99US-0132487.
99US-0132863.
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99US-0127462.
99US-0128234.
99US-0128714.
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                         99US-0123548
99US-0125788
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 99US-0121825
                                                     99US-0126264
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                                                                                                                                               21.4RR-1999;
23.4RR-1999;
28.4RR-1999;
30.4RR-1999;
30.4RR-1999;
40.4MAY-1999;
66.4MAY-1999;
66.4MAY-1999;
70.4MAY-1999;
70.4MAY-1999;
71.4MAY-1999;
71.4MAY-1999;
71.4MAY-1999;
25-FBB-1999;
05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
01-APR-1999;
06-APR-1999;
16-APR-1999;
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25-MAY-1999;
27-MAY-1999;
28-MAY-1999;
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30-7UU-1999
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14-MAY-1999;
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19-MAY-1999;
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21-MAY-1999;
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28-JUN-1
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  The invention relates to isolated polymucleotide (I) and polymerase chain reaction (FRR) primers, oligomers, and for chromosome polymerase chain reaction (FRR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The conditions are also used in diagnostics as expressed sequence tags polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques for restore normal activity of (II) or treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) and of II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in companies for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences of data and products dependent on DNA and and anno acid sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana protein fragment SEQ ID NO: 15445.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                       Claim 20; SEQ ID No 30881; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG15261 standard; Protein; 146 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-FEB-2000; 2000EP-0301439.
                                                                                   Tang YT
                 31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
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44 IHKYHWV 50
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N-PSDB; AAS64709.
                                                                                     Drmanac RT, Liu C,
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                                                             (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-SEP-2000.
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        PR
        13-JUL-1999;
        99US-0143542.

        PR
        15-JUL-1999;
        99US-0144005.

        PR
        16-JUL-1999;
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        PR
        16-JUL-1999;
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        PR
        16-JUL-1999;
        99US-014408.

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        99US-014432.

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        99US-014433.

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        99US-014433.

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        99US-014433.

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        99US-014433.

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        22-JUL-1999;
        99US-014608.

        PR
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        99US-014508.

        PR
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        99US-014508.

        PR
        22-JUL-1999;
        99US-014508.

        PR
        22-JUL-1999;
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PR 04-0CT-1999; 9918-015765.
PR 10-0CT-1999; 9918-015765.
PR 06-0CT-1999; 9918-015765.
PR 11-0CT-1999; 9918-0158369.
PR 11-0CT-1999; 9918-0158369.
PR 11-0CT-1999; 9918-0158329.
PR 11-0CT-1999; 9918-015831.
PR 11-0CT-1999; 9918-0158329.
PR 11-0CT-1999; 9918-0158329.
PR 11-0CT-1999; 9918-0158329.
PR 11-0CT-1999; 9918-016770.
PR 11-0CT-1999; 9918-016789.
PR 1
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Appli Appli Appli 116,

Sequence Sequence Sequence

Sequence Sequence Sequence Sequence Sequence Sequence

US-09-252-991A-28674
US-08-630-820-7
US-08-630-820-7
US-07-925-695-9
US-07-925-695-9
US-08-556-597-116
US-08-308-494A-13
US-09-134-001C-4203
US-09-1182-859-4
US-09-1182-859-4
US-09-1182-859-4
US-09-1182-859-4
US-09-1183-685-6

Appli Appli Appli Appli Appli Appli

Sequence Sequence

Sequence Sequence

Sequence Sequence Sequence

US-09-545-586-5 US-08-468-700-34

ALIGNMENTS

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APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONVERS.

ZIP: 94111-3834

ZIP: 94111-3834

COMPUTER READABLE PORM:
MEDIUM TYPE: Aloppy disk
COMPUTER: PEM PC compatible
OPERATING-SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Townsend and Townsend and Crew LLP o Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRICE APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 14-AUG-1997
PRIOR APPLICATION NUMBER: US 08/911,312
APPLICATION NUMBER: US 08/912 OFF
                                                                                                                                                                                                                                                                                                                                                                         Sequence 118, Application US/08974549A; Patent No. 6166178; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Two Embarcadero
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend a
STREET: Two Embarcade
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     San Francisco
California
US-08-974-549A-118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: S
STATE:
 Sequence 4, Appli
Sequence 14, Appli
Sequence 14, Appli
Sequence 15, Appli
Sequence 15, Appli
Sequence 15, Appli
Sequence 15, Appli
Sequence 3486, Ap
Sequence 5382, Ap
Sequence 570, Appli
Sequence 35, Appli
Sequence 6, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 118, App
Sequence 4, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                    December 16, 2003, 14:11:00 ; Search time 12.3333 Seconds (without alignments) 30.875 Million cell updates/sec
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(cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

(cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

(cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                 GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-974-549A-118
US-08-851-843A-4
US-08-851-843A-4
US-09-853-13-4
US-09-653-13-4
US-09-65-15A-14
US-09-06-726A-6
US-09-08-761A-15
US-09-08-761A-15
US-09-134-01-1348
US-09-134-01-135-135
US-09-31-145-35
US-08-31-145-35
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US-08-928-694-67
US-08-450-842-67
US-08-451-390-67
PCT-US91-06950-67
US-09-413-814-99
                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
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US-08-451-947-67
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                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                            - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                     Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Morin, Garegia B.
APPLICANT: Morin, Greegia B.
APPLICANT: Harley, Calvin
APPLICANT: Harley, Calvin
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6261836el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER: Floppy disk
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION NUMBER: US 08/846,017
FILING DATE: 25-ARR-1997
CLASSIFICATION NUMBER: US 08/846,017
FILING DATE: 25-ARR-1997
CLASSIFICATION NUMBER: US 08/846,017
FILING DATE: 25-ARR-1997
CLASSIFICATION NUMBER: US 08/846,017
                                                                                                                            ATTORNEY AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,4259
REPERRNCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 552 amino acids
TYPE: amino acid
STRANDENNESS: not relevant
TOPOLOGY: not relevant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRICK APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
                          UMBER: US 08/724,643
01-0CT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08854050
Patent No. 2561836
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 55.6
Matches 5; Conservative
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             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 | | | | ::
23 FPHKWRWIL 31
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                                        APPLICATION NUMBER FILING DATE: 01-OCCLASSIFICATION:
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APPLICATION NUMBER: US/08/851,843A FILING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamira, Toru
APPLICANT: Nakamira, Toru
APPLICANT: Morin, Gregg B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Harley, Calvin
APPLICANT: Morin, Cop 1809 B.
TITLE OF INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES: 225
CORRESSEDSUDENCES ADDRESS:
ADDRESSEE: Townsend and Crew LLP
                                                                                                           FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885.
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: APPLE Randolph Ted
REFERENCE/DOCKET NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 36,429
REFERENCE/TOOKET NUMBER: 31,429
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Pred. No. 3.2;
2; Mismatches
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MBER: US 08/844,419
18-APR-1997
FILING DATE: 14-AUG-11...
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: California COUNTRY: United States of America ZIP: 94111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/08851843A Patent No. 6093809 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68.9%;
55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILLING DATE: 18-APR-19
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 55.
Best Local Similarity 55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FPHKWRWIL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 FLHKWHWVV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS
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Gaps
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                                                                                                                                                                                                                                                                                                                                              68.9%; Score 42; DB 4; Length 552; 55.6%; Pred. No. 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-053-197A-14
US-09-053-197A-14
Sequence 14, Application US/09053197A
Sequence 14, Application US/09053197A
Sequence 11, Application US/09053197A
SENERAL INFORMATION:
APPLICANT: Weiner, Joel H.
APPLICANT: Weiner, Raymond J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PROTEIN
TITLE OF INVENTION: SECRETION
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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Pred. No. 24;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
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FILING DATE: 01-APR-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MacKhight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: UALB-03293
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 888 amino acids
                                               INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: San Francisco
STATE: California
COUNTRY: United States of America
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: not relevant TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65.6%;
                                                                                                                                                                                                                                                                                                                                                                                                          5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23 FPHKWRWIL 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 FLHKWHWVV 9
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                            Best_Local Similarity
Matches 5; Conserv
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Pred. No. 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM FC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco CATE: California COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Andrews, William H.
TITLE OF INVENTION: No. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
                                                                                                           REGISTRATION NUMBER: 35.429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0200
INFORMATION POR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
LENGTH: 552 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 15-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
REPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 4
US-09-430-323-4
; Sequence 4, Application US/09430323
; Patent No. 6309867
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Harley, Calvin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68.9%;
55.6%;
     FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                               Randolph T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: not relevant MOLECULE TYPE: protein US-08-854-050-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 FPHKWRWIL 31
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ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REPERRICE/DOCKET NUMBER: UALB-03293
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFRAX: (415) 397-8338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 220 Montgomery Street, Su
CITY: San Francisco
STATE: Callfornia
COUNTRY: United States of America
ZIP: 94104
                                                                                                                                                                        Sequence 615, Application US/09732210 Patent No. 6573361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42 HKWTWII 48
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                                                           48 EWHWVV 53
              4 KWHWVV 9
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Waigel, Detlef
APPLICANT: Salk Institute to Invention:
FILIE OF INVENTION: FLOWERD PLANTS HAVING MODULATED FLOWER DEVELOPMENT
FILIE REPERENCE:
SALKINS. 026A
CURRENT FALING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 1398-04-15
NUMBER OF SEQ ID NOS: 1398-04-15
SOFTWARE: RastSEQ for Windows Version 4.0
LENGTH: 104
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                                                             GENERAL INFORMATION:
APPLICANT: Turner, Raymond J.
APPLICANT: Turner, Raymond J.
APPLICANT: Turner, Raymond J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PROTEIN
TITLE OF INVENTION: SECRETION
NUMBER OF SECURNES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medien & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
STATE: United States of America
ZIP: 94104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63.9%; Score 39; DB 3; Length 104;
83.3%; Pred. No. 38;
tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65.6%; Score 40; DB 4; Length 88; 75.0%; Pred. No. 24; 2; Indels tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                 COMPUTER TEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/085,761A
FILING DATE: 28-MAY-1998
CLASSIFICATION: Peter G.
ATTORNEY/AGBNT INFRAMATION:
NAME: CARTOLI, Peter G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: UALB-03356
TELEPHONE: (415) 397-8338
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 88 amino acids
THENEYA: AMINO ACIDS
THENEYA: AMINO ACIDS
TELEPHORE: AMINO ACIDS
US-09-085-761A-14
; Sequence 14, Application US/09085761A
; Patent No. 6335178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/09060726A Patent No. 6225530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 83.3
Matches 5; Conservative
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Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: unknown MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 LSPWHWWV 11
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FACENT NO. 80.73181

FACENT NO. 80.73181

APPLICANT: Bunkers, Greg J.

APPLICANT: Liang, Jihong

APPLICANT: Liang, Jihong

APPLICANT: Seale, Jeffrey W.

APPLICANT: Seale, Jeffrey W.

APPLICANT: Wu, Younie S.

TITLE OF INVENTION: ALL: fungal Proteins and Methods for Their Use

FILE REFERENCE: 38-21(15036)B

CURRENT APPLICATION NUMBER: US/09/732,210

CURRENT APPLICATION NUMBER: US 60/169,513

PRIOR PILING DATE: 1999-12-07

PRIOR PILING DATE: 1999-12-07

NUMBER OF SEQ ID NOS: 1753

SEQ ID NO 615

LENGTH: 143

TYPE: PRT

ORGANISM: Methanococcus jannaschii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Patent No. 6022952
GENERAL INFORMATION:
APPLICANT: Weiner, Joel H.
APPLICANT: Wriner, Raymond J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PROTEIN TITLE OF INVENTION: SECRETION
TITLE OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
GRODEN: 2007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/09/053,197A
FILING DATE: 01-APR-1998
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5 WHWVV 9
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0
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 15, Application US/09085761A
Patent No. 6335178
GENERAL INFORMATION:
APPLICANT: Weiner, Baymond J.
TITLE OF INVENTION: SECRETION
TITLE OF INVENTION: SECRETION
                                                                                                                                                                                  Score 38; DB 3; Length 79; Pred. No. 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62.3%; Score 38; DB 4; Length 79; 55.6%; Pred. No. 42; 3; Indels tive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/085,761A
FILING DATE: 28 MAY-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSER: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Peter G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: UALB-03356
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 397-8338
INFORMATION FOR REQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 79 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
US-08-411-768B-5
; Sequence 5, Application US/08411768B
; Patent No. 6083712
                                                                              STRANDEDNESS: not relevant
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-053-197A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              not relevant
                                                                                                                                                                                  Query Match
Best Local Similarity 55.6%;
Matches 5; Conservative
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 79 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 55.6
Matches 5, Conservative
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STRANDEDNESS: no
                                                             amino acid
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US-09-085-761A-15
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APPLICANT: Lynn Doucette-Stamm et al
APPLICANTON: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCCCCUS
TITLE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NOS: 5674
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APPLICANT: Olwen Birch
APPLICANT: Olwen Brass
APPLICANT: Johann Brass
APPLICANT: Martin Fuhrmann
APPLICANT: Nicholas Shaw
TITLE OF INVENTION: Biotechnological Method
TITLE OF INVENTION: of Producing Biotin
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSE: Brumbaugh, Graves, Donohue & Raymond
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 62.3%; Score 38; DB 4; I
Best Local Similarity 57.1%; Pred. No. 2.1e+02;
Matches 4; Conservative 2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62.3%; Score 38; DB 100.0%; Pred. No. 77; cive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: WordPerfect
SOFTWARE: WordPerfect
SOFTWARE: WordPerfect
SOFTWARE: WardPerfect
FILING DATE: WAS
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 3124/92
PRIOR APPLICATION NUMBER: CH 2134/93
APPLICATION WHERE: CH 2134/93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-134-001C-3486
; Sequence 3486, Application US/09134001C
; Patent No. 6380370
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INFORMATION FOR SEQ ID NO: 5:
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TYPE: amino acid
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MOLECULE TYPE: protein
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Best Local Similarity
Matches 5; Conserv
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APPLICANT: Mahajan-Miklos, Shalina
APPLICANT: Tan, Man-Wah
APPLICANT: Tan, Man-Wah
APPLICANT: Tan, Man-Wah
APPLICANT: Tao, Hul.
APPLICANT: Tao, Hul.
APPLICANT: Taongalis, John
TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
FILE REFERENCE: 00786/361002
CURRENT FILING DATE: 1992-11-25
CURRENT FILING DATE: 1997-11-25
PRIOR APPLICATION NUMBER: 60/66,517
PRIOR APPLICATION NUMBER: 60/66,517
PRIOR PELING DATE: 1997-11-25
NUMBER OF SEQ ID NOS: 437
SEQ ID NO 407
LENGTH: 246
TYPE: PRI PREUDMONER ABENDAND AND ASSOCIATED ASS
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                                                                                                                                                                                                                                                                                                    APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ·;
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                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60.7%; Score 37; DB 4; I 62.5%; Pred. No. 1.3e+02; rative 2; Mismatches 1;
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LOCATION: (B) LOCATION 1...191

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SEQUENCE DESCRIPTION: SEQ ID NO: 5382:

US-09-107-532A-5382
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                                                                                                                                                                                         US-09-107-532A-5382
; Sequence 5382, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 62.5
Matches 5; Conservative
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167 LDRWHWI 173
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                     2 LHKWHWV 8
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RESULT 14
US-09-637A-407
Sequence 407, Application US/09199637A
Patent No. 6355411
GENBRAL IRPORMATION:
APPLICANT: Ausubel, Frederick
APPLICANT: Goodman, Howard M.

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US-09-328-352-5670

i Sequence 5670, Application US/09328352

j Patent No. 656258

j Fatent No. 656258

j TITLE OF INVENTION:

i TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

j TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

j TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

j CURRENT APPLICATION NUMBER: US/09/328,352

j CURRENT FILE REFERENCE: GTC99-03PA

j CURRENT FILING DATE: 1999-06-04

j NUMBER OF SEQ ID NOS: 8252

j SEQ ID NO 5670

j ENGTH: 442
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                                                        Gaps
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60.7%; Score 37; DB 4; Length 246; 80.0%; Pred. No. 1.6e+02; ive 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5670
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Matches 5; Conservative
                                                           4; Conservative
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US-09-870-089B-7
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Sequence 9, Appli
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Sequence 7554, Ap
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                                                                                  December 16, 2003, 14:18:11; Search time 22.1667 Seconds (without alignments) 75.512 Million cell updates/sec
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/ cgn2 6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
/ cgn2 6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
/ cgn2 6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
/ cgn2 6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
/ cgn2 6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
/ cgn2 6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
/ cgn2 6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-870-089B-9
US-09-843-676-4
US-09-766-253-4
US-10-053-758-4
US-10-053-758-4
US-10-054-611-4
US-10-054-611-4
US-10-106-698-4974
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US-09-870-089B-3
US-10-029-386-33052
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US-09-291-809C-8
US-09-845-849-8
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                                                                                                                                                                                                                                             684280 seqs, 185983659 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                     Published_Applications_AA:*
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                                                         protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Perfect score:
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Maximum DB s
                                                           OM protein
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No.
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Sequence 56, Appl Sequence 1146, Appl Sequence 1220, Appl Sequence 12, Appl Sequence 72, Appl Sequence
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APPLICANT: Charles A. MICOLEtte; TITLE OF INVENTION: A. MICOLETTE; FILE REFERENCE: 66126891209900; CURRENT APPLICATION NUMBER: US/09/870,089B; CURRENT FILING DATE: 2001-05-30; NUMBER OF SEQ ID NOS: 14
SOFTWARES FASISEQ for Windows Version 3.0
; SEQ ID NO?; LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Charles A. Nicolette
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS FOR OVARIAN CANCER
FILE REFERENCE: 68126881209900
CURRENT APPLICATION NUMBER: US/09/870,089B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 9;
                                                                  US-10-156-761-9146
US-10-156-761-9146
US-10-156-761-9120
US-10-137-907-72
US-10-140-018-72
US-10-140-912-72
US-10-140-922-72
US-10-140-922-72
US-10-140-922-72
US-10-140-922-72
US-10-140-922-72
US-10-140-924-72
US-10-141-702-72
US-10-141-702-72
US-10-142-432-72
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US-10-145-833-72
US-10-145-833-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 61; DB 12;
100.0%; Pred. No. 6.1e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 9, Application US/09870089B
; Publication No. US20030175252A1
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0S-09-870-089B-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPÉ: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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Gaps

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Score 42; DB 10; Length 552;
Pred. No. 2.7e+02;
2; Mismatches 2; Indels
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COMPUTER: IBM PC Compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/766,253
FILING DATE: 19-Jan-2001
CLASSIFICATION: -Unknown>
PRIOR APPLICATION NUMBER: 08/846,017
FILING DATE: 1997-04-25
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: APPLICATION NUMBER: 36,429
ATTORNEY/AGENT INFORMATION:
NAME: APPLICATION NUMBER: 36,429
FILING DATE: NUMBER: 36,429
                                                                Score 42; DB 10; Length 552;
Pred. No. 2.7e+02;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Harley, Calvin
Andrews, William H.

TITLE OF INVENTION: No. US20020187471A1el Telomerase
NUMBER OF SEQUENCES: 171
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: not relevant TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/09766253 Publication No. US20020187471A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Morin, Gregg B.
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55.6%;
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                                                                    68.9%;
55.6%;
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                    Query Match 68.9
Best Local Similarity 55.6
Matches 5; Conservative
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23 FPHKWRWIL 31
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Best Local Similarity
Matches 5; Conserval
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                                                                                                                                                                                                                                                                              RESULT 4
US-09-766-253-4
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US-09-843-676-4
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Pred. No. 6.1e+05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Cech, Thomas R.

APPLICANT: Cech, Thomas R.

ARkamura, Joachim
Nakamura, Toru
Chapaman, Karen B.

Morin, Gregg B.

Harley, Calvin
Andrews, William H.

TITLE OF INVENTION: No. US20020164786Alel Telomerase
NUMBER OF SEQUENCES: 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTATION TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/09/843,676
FILING DATE: 26-Apr-2001
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 552 amino acids
TYPE: amino acid
STRANDEDNESS: No. US20020164786A1 Relevant
TOPOLOGY: No. US20020164786A1 Relevant
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REGISTRATION NUMBER: 36,429
REGISTRATION INFORMER: 015389-002930US
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/654,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: United States of America
       CURRENT FILING DATE: 2001-05-30
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/09843676
Patent No. US20020164786Al
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                         CTHER INFORMATION: ATF4/CREB-2 US-09-870-089B-9
                                                                                                                                                                                                                                                           91.8%;
88.9%;
                                                                                                                             TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94111
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                           8; Conservative
                                                                                                                                                                                                                                                                                                                                                     1 FLHKWHWVV 9
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-843-676-4
                                                                                SEQ ID NO 9
LENGTH: 9
                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                             Matches
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Gaps

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APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chaman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20030032075Alel Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READBLE FORM:

MEDIUM TYPES Flopy disk

COMPUTER: IBM PC compatible

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/053,758

FLING DATE: 18-Jan-2002

CLASSIFICATION DATA:

APPLICATION NUMBER: US/08/854,050

FLING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

ATTORNEY AGENT: INFORMATION:

ATTORNEY AGENT: INFORMATION:

ATTORNEY AGENT: INFORMATION:

ATTORNEY AGENT: INFORMATION:

ATTORNEY AGENT: INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: California COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (415) 576-0200
Sequence 4, Application US/10053758 Publication No. US20030032075A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (415) 576-0300
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                                                                                                                               APPLICANT: Linguer, Joachim
APPLICANT: Cech, Thomas R.
APPLICANT: Cech, Thomas R.
APPLICANT: Cech, Thomas R.
APPLICANT: Makamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Chapman, Karen B.
APPLICANT: Chapman, Karen B.
APPLICANT: Marin, Greegy B.
APPLICANT: Marin, Greegy B.
APPLICANT: Harley, Calvin
APPLICANT: Harley, Calvin
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: NO. US20030009019A1e1 Telomerase
NUMBER OF SEQUENCES: 223
CORRESPONDENCE ADDRESS:
ADDRESSEE: Two Embarcadero Center, &th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ibb PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PREPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION STA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 06-MAY-1997
CLASSIFICATION STA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION STA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 10-OCT-1996
CLASSIFICATION NUMBER: US 08/76-0200
TELERHOM: (415) FAC-0200
                                                          Sequence 4, Application US/09438486
Publication No. US2003009901941
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: not relevant TOPOLOGY: not relevant MIDECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFACE (415) 576-0300
TELEFACE (415) 576-0300
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 552 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 FPHKWRWIL 31
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                                                                                                                                                                                    Score 42; DB 15; Length 33.
Pred. No. 2.7e+02;
Transa 2; Indels
                                                     TYPE: amino acid
STRANDEDNESS: No. US20030032075A1 Relevant
TOPOLOGY: No. US20030032075A1 Relevant
                                                                                                                        MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/10054295; Publication No. US20030044953A1; GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim; Nakamura, Toru
                                      LENGTH: 552 amino acids
INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                       Query Match 68.9%;
Best Local Similarity 55.6%;
                                                                                                                                                                                                                                                5; Conservative
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23 FPHKWRWIL 31
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RESULT 6 US-10-053-758-4

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NES-10-106 6-98-4974

Sequence 4974, Application US/10106698

Sequence 4974, Application US/10106698

Publication No. US20030109690A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TILE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide

FILE REFERENCE: PA005P1

CURRENT FILING DATE: 2002-02-27

FRICR APPLICATION NUMBER: US/10/106,698

FRICR FILING DATE: 2000-09-28

FRICR FILING DATE: 1999-09-29

PRIOR FILING DATE: 1999-09-29

PRIOR FILING DATE: 1999-11-03

NUMBER OF SEQ ID NOS: 8564

SOFTWARE: PRICEITING VET 3.0

STORTMARE: PRICEITING VET 3.0
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                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/10/054,611
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/854,050
FILING DATE: «Unknown» 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 10-0CT-1996
ATTORNEY/AGENT INFORMATION:
NAME: APPLE 01-0CT-1996
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 36,429
REGISTRATION NUMBER: 36,429
RECIONALICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHRACTERISTICS:
LENGTH: 552 amino acids
STRANDEDNESS: No. US20030059787A1 Relevant
TOPOLOGY: No. US20030059787A1 Relevant
STREET: Two Embarcadero Center, 8th Floor
                           CITY: San Francisco
STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 55.6
Matches 5; Conservative
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ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: MISC_FEATURE
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23 FPHKWRWIL 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: NO. US20030059787Alel Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
               Morin, Gregg B.
Harley, Calvin
Andrews, William H.
OF INVENTION: No. US20030044953Alel Telomerase OF SEQUENCES: 225
                                                                                                                                                                                                                                                                                                                      COMPUTER EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUBER: US/10/054,295
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                       ADDRESSE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US20030044953Al Relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REGISTRATION NUMBER: 36,429
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 552 amino acids
TYPE: amino acids
TYPE: amino acid
TYPE: amino acid
STRANDENESS: No. US20030044953A1 Relevant
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-054-295-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/854,050
FILING DATE: -CUNKNOWN:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                             COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
US-10-054-611-4
Sequence 4, Application US/10054611
; Publication No. US20030059787A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
            Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Morin, Gregg B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                        TITLE OF INVENTION: NO. NUMBER OF SEQUENCES: 22 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 55.6
Matches 5; Conservative
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APPLICANT: Ruben et al.

TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
TITLE REPERENCE: PA005P1
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-28
PRIOR PELIONION NUMBER: US 60/157,137
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR APPLICATION NUMBER: PAGENTIN Ver. 3.0
SEQ ID NO 7554
                                                                                                                                                                                 Sequence 8, Application US/09845849
; Sequence 8, Application US/09845849
; Patent No. US2002002995A1
; GENERAL INFORMATION:
    APPLICANT: THE SALK INSTITUTE FOR BIOLOGICAL STUDIES
; APPLICANT: WEIGEL, Detlef
; APPLICANT: KARDAILSKY, IGOR
; TITLE OF INVENTION: FLOWERING LOCUS T (FT) AND GENETICALLY
; TITLE OF INVENTION: PLOWERING LOCUS T (FT) AND GENETICALLY
; TITLE OF INVENTION: NUMBER: US/09/845,849
; CURRENT APPLICATION NUMBER: US/09/845,849
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 09/060,726
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FREEER for Windows Version 4.0
; TENTING DATE: 100 NOS: 13
; SEQ ID NOS: 13
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NAME/KEY: MISC_FEATURE
LOCATION: (65)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
OTHER INFORMATION: As equals any of the naturally occurring L-amino acids
NAME/KEY: Misc_FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (85) OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: MISC_FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (98)

CTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-10-106-698-7554
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83.3%; Pred. No. 1.8e+02;
.ive 1; Mismatches 0; Indels
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Sequence 7554, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 83.5.
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50 EWHWVV 55
                                                                  50 EWHWVV 55
              4 KWHWVV 9
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APPLICANT: Strittmater, Warren
APPLICANT: Strittmater, Warren
APPLICANT: Nagai.
APPLICANTON: COMPOUNDS THAT SELECTIVELY BIND TO EXPANDED POLYGLUTAMINE REPEAT
TITLE OF INVENTION: AND METHODS OF USE THEREOF
FILE REFERENCE: 5405.242
CURRENT APPLICATION NUMBER: US/09/780,070
CURRENT FILING DATE: 2001-02-09
PRIOR PADLICATION NUMBER: 60/189,781
PRIOR PILING DATE: 2000-03-16
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PATENT OF SEQ ID NOS: 40
SOFTWARE: PATENT OF SEQ ID NOS: 40
SOFTWARE: ALENTIN VETSION 3.0
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SERVED Detlef Weigel
APPLICANT: Salk Institute
STILLE OF INVENTION: FLOWERING LOCUS T (FT) AND GENETICALLY
TITLE OF INVENTION: US/09/291,809C
TITLE OF INVENTION: US/09/291,809C
CURRENT APPLICATION NUMBER: US/09/291,809C
CURRENT FILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-04-15
SPRIOR FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 106
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; LOCATION: (37)
; CTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-4974
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                                                                                                                          Query Match 65.6%; Score 40; DB 15; Length 41; Best Local Similarity 50.0%; Pred. No. 62; Matches 4; Conservative 3; Mismatches 1; Indels
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Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 11;
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Pred. No. 29;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 21, Application US/09780070; Patent No. US20020009752A1; GENERAL INFORMATION:
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US-09-291-809C-8
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80.0%;
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US-09-780-070-21
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27 LHPWNWII 34
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Best Local Similarity
Matches 4; Conserv
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Search completed: December 16, 2003, 14:41:06 Job time : 23.1667 secs
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Publication No. US20030194704A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: PENNENDIN: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REPERENCE: ADONICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT PILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 33052
LENGTH: 19
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US-069B-3
US-06-870-069B-3

Sequence 3, Application US/09870089B

Publication No. US20030175252A1

GENERAL INFORMATION:

APPLICANT: Charles A. Nicolette

TITLE OF INVENTION: THERAPEUTIC COMPOUNDS FOR OVARIAN CANCER

TITLE REFERENCE: 681268B1209900

CURRENT PILIOS DATE: 2001-05-30

NUMBER OF SEQ ID NOS: 14

SEQ ID NO 3

LENGTH: 9

LENGTH: 9
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60.7%; Score 37; DB 12; Length 19;
Best Local Similarity 66.7%; Pred. No. 84;
Matches 4; Conservative 2; Mismatches 0; Indels
                       Query Match 62.3%; Score 38; DB 15; Length 98; Best Local Similarity 55.6%; Pred. No. 2.38+02; Matches 5; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:

OTHER INFORMATION: MAP TO Z49918.1

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.85

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.91

US-10-029-386-33052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 60.7%; Score 37; DB 12; Length 9; Best Local Similarity 66.7%; Pred. No. 6.1e+05; Matches 6; Conservative 1; Mismatches 2; Indels
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; OTHER INFORMATION: ATF4/CREB-2
US-09-870-089B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
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FLQRWFWLV 13
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4 VNKWHW 9
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US-10-029-386-33052
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GenCore version 5.1.6
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OM protein - protein search, using sw model

December 16, 2003, 14:10:15 е :: Run

; Search time 10.3333 Seconds (without alignments)
83.760 Million cell updates/sec

US-09-870-089B-7 Perfect score:

1 FLHKWHWVV 9 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 sed Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

4:94 PIR ' Database :

1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	conserved hypothet		vif protein - simi	ρ H	ATP-dependent RNA	hypothetical prote		hypothetical prote		Н	0	hypothetical prote	Ω	hypothetical prote		٦		polyprotein - infe	conserved hypothet	hypothetical prote	conserved hypothet	hypothetical prote	hypothetical prote	ρ	conserved hypothet	enterohemolysin 2	hypothetical prote	_	_
SUMMARIES	ΩI	876	G82786	S28082	F95871	848	S72850	E87075	G75174	H71039	T28923	E64359	A70014	C75311	T06656	AG2462	T20609	T21891	T00327	H64559	A71948	Q3ECBA	C90735	D85585	AF0596	T36855	JN0846	A99775	D85637	AF2129
	DB	1	N	N	Ŋ	N	Н	N	N	ď	N	N	7	~	~	N	~	7	7	H	N		N	N	~	(1	N	N	7	7
	Length	209	218	172	œ	0	88	95	9	295	v	143	145	159	210	259	795	1059	3085	79	79	158	158	158	158	179	193	ഹ	257	ч
ok	Query Match	l N	75.4	68.9	67.2	7.	ď.	9.59	S.	Š	5.	ω.	ω,	ë.	•	m.	س	63.9	63.9	ä	ά.	ď.	ď	ď.	ς.	•	•	62.3		62.3
	Score	4	46	42	4.1	41	40	40	40	40	40	39	39	39	39	39	39	39	39	38	38	38	38	38	38	38	38	38	38	38
	Result No.		7	٣	4	ស	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

hypothetical prote	probable membrane	sodium-dependent t	probable acid-CoA	probable exported	hemocyanin chain a	bromodomain protei	hypothetical prote	metal-regulated pr	hypothetical prote	hypothetical prote	apoptosis specific	hypothetical prote	replication-associ	aspartate dehydrog	aspartate dehydrog
F64022	S61598	D69902	G70604	AB0005	BHTLA	T49984	C90605	G69660	T29758	T49291	T40482	G64426	JC1418	E86621	G72002
8	7	~	~	C3	Н	7	~	~	~	~	~	N	~	7	03
367	380	445	507	569	631	678	134	153	214	259	261	294	312	333	333
62.3	62.3	62.3	62.3	62.3	62.3	62.3	60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.7
38	38	38	38	38	38	38	37	37	37	37	37	37	37	37	37
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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C. Species: Caulobacter crescentus
C. Species: Caulobacter crescentus
C. Species: Caulobacter crescentus
C. Species: Caulobacter crescentus
C. Species: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C. Accession: A87628
R. Mierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Koln, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C. AyTitle: Complete Genome Sequence of Caulobacter crescentus.
A. Title: Complete Genome Sequence of Caulobacter crescentus.
A. Accession: A87628

A, Status: preliminary A, Molecule type: DNA

A;Residues: 1-209 <STO> A;Cross-references: GB:AE005673; NID:g13424707; PIDN:AAK25021.1; GSPDB:GN00148

A; Gene: CC3059 C; Genetics

C; Superfamily: Dernococcus radiodurans hypothetical protein DR1792

Gaps .; 0 Length 209; Indels ; 75.4%; Score 46; DB 2; 71.4%; Pred. No. 3.9; tive 2; Mismatches Query Match Best Local Similarity 71.4 Matches 5; Conservative

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RESULT 2

conserved hypothetical protein XF0597 [imported] - Xylella fastidiosa (strain 9a5c) C;Species: Xylella fastidiosa C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000

C;Accession: G82786
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequenture 406, 151-157, 200
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: G8786

A;Status: preliminary

A; Molecule type: DNA

A;Residues: 1-218 <SIM> A;Cross-references: GB:AE003905; GB:AE003849; NID:g9105456; PIDN:AAF83407.1; GSPDB:GNO

AjExperimental gource: strain 9a5c Risimson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.B.A.; Carraro, D.M.; Carrer, as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000 A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frol

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67.2%;
llarity 62.5%;
Conservative
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Matches 5; Conservative
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128 LHRFHWIV 135
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Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
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A; Map position: 2
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J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.A; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.P. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sal, R.G.; Santelli, R.V.; Sawabak M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z.A; C.Genetics:
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R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endc A;Reference number: A95842; MUID:21396508; PMID:11481431
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A;Nolecule type: DNA
A;Nolecule type: DNA
A;Nolecule type: DNA
A;Residues: 1-582 <KUR>
A;Cross-references: GB:AL591985; PIDN:CAC48638.1; PID:g15140110; GSPDB:GN00167
A;Experimental source: strain 1021, megaplasmid pSymB
A;Experimental source: strain 1021, megaplasmid pSymB
B;Galibert, F:; Finnan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
Bcience 293, 668-722, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, B.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
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C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 24-Nov-1999
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 24-Nov-1999
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 24-Nov-1999
R;Pacsion: S;B080
A;Fitle: Sequence 0; A; Maki, N; Fukasawa, M; Miura, T; Speidel, S; Cooper, Nature 341, 539-541, 1989
A;Fitle: Sequence of a novel simian immunodeficiency virus from a wild-caught African ma;Reference number: S28080; MUID:90015168; PMID:2797181
A;Reference number: S28080; MUID:90015168; PMID:2797181
A;Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A.Residues: 1-172 <TSUs
A.Cross-references: GB:M27470; EMBL:X15781; NID:g334683; PIDN:AAB49570.1; PID:g334688
A.Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1989
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C;Superfamily: Deinococcus radiodurans hypothetical protein DR1792
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                                                                                                                                                                                                                                                                                                                                                                                                                          75.4%; Score 46; DB 2; Length 218; 71.4%; Pred. No. 4;
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A,Gene: vif
C,Superfamily: AIDS vif protein
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Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
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Tre-dependent RNA helicase [imported] - Arabidopsis thaliana Cispecies: Arabidopsis thaliana (mouse-ear cress) Cibate: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 C;Accession: 684832 A;Accession: 684832
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A,Title: The composite genome of the legume symbiont Sinorhizobium meliloti. A,Reference number: A96039; MUID:21368234; PMID:11474104
A,Contents: annotation
C,Genetics:
A,Gene: SMD20248
A;Genome: plasmid
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C;Species: Mycobacterium leprae
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 23-Mar-2001
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                                                                                                                                                                                                                                                                                                                                                        Score 41; DB 2; Length 582;
Pred. No. 61;
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C,Superfamily: conserved hypothetical secreted protein HP0320
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K;Smith, D.R.; Robison, K.
submitted to the EMBL Data Library, November 1993
A;Description: Mycobacterium leprae cosmid B2126.
A;Reference number: S72585
A;Accession: S72850
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-88 <SMI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
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Gaps

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ribosomal protein L15 - Methanococus jannaschii
C;Species: Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Date: 113-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: E64359
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, rsoit, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borcodovsky, M.; Klank, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C A;Authors: Kaine, B.P.; Panordovsky, M.; Klank, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C A;Athler: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii A;Reference number: A64359
A;Rering, D.C., Shang, MUID:96337999; PMID:8688087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Map position: 1
Thirrons: 43/2; 111/1; 185/3; 221/3; 298/2; 327/3; 364/2; 411/2; 500/1; 595/1; 643/3; 7
2; 1594/1; 1638/3
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A;Molecule type: DNA
A;Residues: 1-295 «KMA»
A;Residues: 1-295 «KMA»
A;Cross-references: GB:AP000006; NID:g3236133; PIDN:BAA30720.1; PID:g3258037
A;Experimental source: strain OT3
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank C;Genetics:
A;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, April 1997
A, Description: The sequence of C. elegans cosmid C48B6.
A, Reference number: Z20544
A, Reference number: Z20544
A, Accession: T28923
A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Molecule type: DNA
A, Residues: 1-1663 < MIN>
A, CROSS references: EMBL:U97189; PIDN: AAC48166.1; GSPDB:GN00019; CESP:C48B6.6
C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T28923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65.6%; Score 40; DB 2; Length 1663; 44.4%; Pred. No. 2.5e+02; tive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 63.9%; Score 39; DB 2; Length 143; Best Local Similarity 57.1%; Pred. No. 31; Matches 4; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                  Length 295;
                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein C48B6.6 - Caenorhabditis elegans
                                                                                                                                                                                                                                                         5
                                                                                                                                                                                                                                                  Score 40; DB
Pred. No. 44;
0; Mismatches
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C;Superfamily: rat ribosomal protein L27a
                                                                                                                                                                                                                                                  Query Match 65.6%;
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 65.6
Best Local Similarity 44.4
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                          86 FFHKWSW 92
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                                                                                                                                                                                                                                                                                                                                                                             1 FLHKWHW 7
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C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 21-Jul-2000
C;Accession: H71039
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
M.; Ohfu:u, Y.; Punahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A;Reference number: A71000; MUID:98344137; PMID:9679194
                                                                                                                                                                                                        R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho
R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
eam, M.A.; Rutherford, K.M.
                                                                                                                                                                                                                                                                                                                Nature 409, 1007-1011, 2001
Ayduthors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R, anonymous, Genoscope submitted to the EMBL Data Library, July 1999 A, Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru A, Reference number: A75001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AJ248284; GB:AL096836; NID:g5457730; PIDN:CAB49478.1; PID:g545798
A;Experimental source: strain Orsay
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                                                                                                          hypothetical protein PAB1992 - Pyrococcus abyssi (strain Orsay)
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
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C;Superfamily: conserved hypothetical secreted protein HP0320
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                                                                                             probable secreted protein [imported] - Mycobacterium leprae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65.6%; Score 40; DB 2;
illarity 75.0%; Pred. No. 14;
Conservative 0; Mismarches
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Pred. No. 39;
0; Mismatches
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Best Local Similarity 71.4
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 LHKWHWVV 9
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Accession: E87075
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-95 <STO>
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A,Gene: PAB1992
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2 LHKWHWVV 9

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Cjāccession: AG2462
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yamada, M.; Tabata, S. DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anat A;Reference number: AB1807; WUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C, Accession: T06656
R; Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X. submitted to the Protein Sequence Database, April 1999
A; Reference number: 215791
A; Accession: T06656
A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Cross-references: GB:BA000019; PIDN:BAB76954.1; PID:g17134394; GSPDB:GN00179
A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                      hypothetical protein T6G15.90 - Arabidopsis thaliana
C,Species: Arabidopsis thaliana (mouse-ear cress)
C,Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 22-Oct-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:AL049656; GSPDB:GN00062; ATSP:T6G15.90 A;Experimental source: cultivar Columbia; BAC clone T6G15
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Conservative
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Best Local Similarity
5; Conserve
     11 VHPWHWWV 18
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-259 <KUR>
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Bern, S. D. Emmerson, P.T. Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.; Entiach, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler, Anthors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler, D.; Fritz, C.; Fujita, M.; Fuline, A.; Hosono, S.; Hullo, M.F.; Atthors: Lauber, J.; Lazarevic, V.; Lek, S.H.; Farro, V.; Pohl, T.M.; Porteelle, A.; Ravielle, C.; Rocha, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sero, Authors: Yoshikawa, H.; Tomakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, Huthors: Yoshikawa, H.; Jumatein, B.; Yoshikawa, H.; Danchin, A.; Tosato, V.; Voshida, R.; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

Arecondon. Annakoshi, A.; Aller, A.; Aller
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(5,Species: Deinococcus radiodurans
(5,Species: Deinococcus radiodurans
(5,Accession: C75311
(5,Accession: C75311
(7,1)
(7,1)
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A;Molecule type: DNA
A;Reaidues: 1-159 <WHI>
A;Cross-references: GB:AE002048; GB:AE000513; NID:g6459929; PIDN:AAF11686.1; PID:g645993
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),Cross-references: GB:Z99120, GB:AL009126; NID:g2635613, PIDN:CAB15183.1; PID:g2635690
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                                                                                                                                                                                                                                                                                                                                                                       pothetical protein yukJ - Bacillus subtilis
Species: Bacillus subtilis
Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
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Q8k9x4 buchners ap
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Q9x794 escherichia
Q9x92 streptomyce
P4132 haemophilus
P53053 saccharomyc
Q9nf16 eurypelma c
P14750 eurypelma c
P14750 bacillus su
P39624 haemophilus
P39624 eurypelma c
Q86234 haemophilus
P3964 bacillus su
Q13686 homo sapien
P39647 androctonus
Q9nfh9 eurypelma c
P02242 eurypelma c
Q9nfh9 eurypelma c
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Q9nf15 eurypelma c
Q18115 caenorhabdi
P31630 cowpea seve
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P54047 methanococo
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                                                                                                   December 16, 2003, 14:06:35; Search time 5.6667 Seconds (without alignments) 74.689 Million cell updates/sec
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Q9nu22
P80879
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P23000
Q01109
P49833
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                            127863 seqs, 47026705 residues
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R115 METJA

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Y160 BUCAP

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Q10295 schizosacch Q8x1p0 erysiphe gr Q9c169 neurospora Q00273 epizoctic h O54782 mus musculu Q9z0t6 mus musculu P2661 h genome po Q10703 mycobacteri P18512 mus musculu P53834 saccharomyc Q8yfr3 brucella me Q41020 papaver som		cein).	irus.	., Miura T., Speidel S., i M.; i M.; im.; from a wild-caught ISOLATE.	is produced through a collaboration ormatics and the EMBL outstation. There are no restrictions on its ong as its content is in no way oved. Usage by and for commercial (See http://www.isb-sib.ch/announce/).	SFCB CRC64;	Length 172; 1; Indels 0; Gaps 0;		;} tatA/E homolog.
566 1 PAP SCHPO 718 1 CATA ERYGR 719 1 CATA ERYGR 719 1 VEZ EHVVI 1018 1 M2BZ MOUSE 2126 1 PKDR MOUSE 3033 1 POLG HVVJ8 83 1 TATA MYCTU 116 1 HV61 MOUSE 153 1 YN21 YEAST 154 1 RNH BRUME 158 1 MLPZ PAPSO	ALIGNMENTS	STANDARD; PRT; 172 AA. 1. 19, Created) 1. 19, Last sequence update) 1. 19, Last annotation update) 1. 19, Last protein) (Q protein)	VIF. Simian immunodeficiency virus (isolate GB1). Simians, Retroid viruses; Retroviridae; Lentivirus (CB1_TaxID=11732;	=2797181; Maki N., N., Gojobori ian immunode VIRUS INFEC	ry is copyright. Institute of Bionic ormatics Institute. Institutions as 1 tatement is not remarked agreement license agreement license agreement	11, 11al_infect. NINFFCT. 1_infect; 1, 499 MW; 205E7BDDE626	68.9%; Score 42; DB 1; 62.5%; Pred. No. 8.6; ative 2; Mismatches	20 V	YCLE TATA MYCLE STANDARD; PRT; 88 AA. 54079; 1-007-1996 (Rel. 34, Created) 8-FEB-2003 (Rel. 41, Last annotation update) ec-independent protein translocase protein tat
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ၟ		ULT 1 SIVGB STANDARD; P22383; 01-AUG-1991 (Rel. 19, Cre. 01-AUG-1991 (Rel. 19, Las' 01-AUG-1991 (Rel. 19, Las' Virion infectivity factor	VIF. Simian immunodefi Viruses; Retroid NGBI_TaxID=11732;	MEDLINE=90015168; PubMed TSUJIMOLO H., Hasegawa A TSUJIMOLO H., Hasegawa A Cooper R.W., Moriyama E., Sequence of a novel sim African mandrill."; Mature 341:539-541(1989) hature FUNCTION: DETERMINES: -1- MISCELLANEOUS: THIS	his SWISS-I tetween the he European se by noi odified an ntities rec	EMBL; M27470; AAB49579 InterPro; IPR000475, V Pfam; PF00559; Vif. 1. PRINTS; PR00349; VIRXO PRODOM; PD000064; Vira AIDS.	atc]	2 LHI : 19 IEI	TT 2 MXCLE TATA MYCLE P54079; 01-0CT-1996 28-FEB-2003 Sec-independ
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EMBL; U67497; AAB98466.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 HKWHWVV 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI TaxID=98794;
 RPL15P OR MJ0477
                                                                       NCBI_TaxID=2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BUCAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Y160_BUCAP
ID _Y160_BUCA
AC Q8K9X4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 4
 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                 BEARING SIGNAL PEPTIDES WITH THE TWIN ARGININE CONSERVED MOTIF STTR. F.L.Y. THIS SEC-INDEPENDENT PATHWAY IS TERMED TAT FOR TWIN-ARGININE TRANSLOCATION SYSTEM, THIS SYSTEM MAINLY TRANSPORTS PROTEINS WITH BOUND COFACTORS THAT REQUIRE FOLDING PRIOR TO EXPORT
                                                                                                                                                                                               STRAIN-IN;

MEDLINE-21128732; PubMed=11234002;

Cole S.T., Eiglmeder K., Parkhill J., James K.D., Thomson N.R.,

Wheeler B.T., Eiglmeder K., Garnier T., Churcher C., Harris D.,

Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,

Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,

Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,

Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,

Ruther S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,

Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                             "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
-!- FUNCTION: REQUIRED FOR CORRECT LOCALIZATION OF PRECURSOR PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
0
                      Mycobacterium leprae.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; ALO35310; CAA22941.1; -.
EMBL; ALO35310; CAA22941.1; -.
EMBL; ALS83921; CAC31712.1; ALT_INIT.
Leproma, ML1331; -.
HAMAP; MF 00236; -; -.
HAMAP; MF 00236; -; -.
InterPro; IPR006312; Tata_E.
Pfam, PF02416; MtA Hcf106.
ITGREPAMS; TIGROL411; tataB: -.
TIGREPAMS; TIGROL411; tataB: 1.
Transport; Protein transport; Translocation; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 40; DB 1; Length 88; Pred. No. 9.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                             Smith D.R., Robison K.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
ML1331 OR MLCB2533.27 OR U2126B OR B2126_C1_182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BI S.M.LARILII).
(BI S.M.LARILIII).
SUBCELLIARILIY: BELONGS TO THE TATA/E FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97F8C81009F7CAC8 CRC64;
                                           Corynebacteringae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-1996 (Rel. 34, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update) 50S ribosomal protein L15P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last seqn
16-OCT-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65.6%;
ilarity 75.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88 AA; 9824 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U00017; AAA17190.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LSPWHWVV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LHKWHWVV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome.
TRANSMEM 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 9
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P54047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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ID RLIS_ME

AC P54047;

DT 01-OCT-

DT 16-OCT-

DE 50S rik
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RESULT 3

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                                                                                                                                                                                                            SEQUENCE FROM N.A.

STRAIN=JAL-1 / DSM Z661 / ATCC 43067;

STRAIN=JAL-1 / DSM Z661 / ATCC 43067;

MEDLINE=96337999; PubMed=868087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Scotton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Puhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Shith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Buchnera aphidicola (subsp. Schizaphis graminum).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Buchnera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22084549; PubMed=12089438; Tamas I., Klasson A.-S., Tamas I., Klasson L., Cabaeck B., Nacelund A.K., Eriksson A.-S., Wernegreen J. J., Sandstroem J.P., Moran N.A., Andersson S.G.E.; "50 million years of genomic stasis in endosymbiotic bacteria."; Science 296:2376-2379(2002).
-! SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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Methanococcus jannaschii.
Archaea; Euryarchaeota; Methanococci; Methanococcales;
Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ribosomal protein; Complete_proteome.
SEQUENCE 143 Aa; 16107 MW; 2A78A8ABA578FF87 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
PUSCHECICAL Protein BUSG160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGR, MJ0477, -.
INTERPRO, IRPROILISE, RIDOSOMAL_LIS.
PERM, PF00256, LIS, 1.
PROSITE, PS00475, RIBOSOMAL_LIS; 1.
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

Li Y., Feng J., Templeton J.W.;

Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL

-!- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL

CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A

G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND

MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY

AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY (BY
                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos taurus (Bovine).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                         63.9%; Score 39; DB 1; Length 310; 66.7%; Pred. No. 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
1-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last amontation update)
High affinity interleukin-8 receptor B (IL-8R B) (CXCR-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U19947; AAA84996.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRHODOPSN.
PROSITE; PS502627; G_PROTEIN RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                        Interpro; IPR005496; TerC.
Pfam; PF03741; TerC; 1.
Hypothetical protein; Transmembrane; Complete proteome.
                                                                                                                                                                                                                                                                                                                         POTENTIAL.
44B75CDED6B47004 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          360 AA
                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (Se
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                      or send an email to license@isb-sib.ch)
                                                                                                                                                                                             POTENTIAL. POTENTIAL.
                                                                                                                                                                                POTENTIAL
                                                                                                                                                                                                                                                                                                        POTENTIAL
                                                                                                       EMBL; AE014091; AAM67728.1; -.
                                                                                                                                                                                                                                                                                                                                          36938 MW;
                                                                                                                                                                                                                                                                                                                                                                                             66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                      228
256
284
310 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   132 KWHWIL 137
                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 4, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 KWHWVV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEBRE OR CXCR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IL8B BOVIN
Q28003;
                                                                                                                                                                                                TRANSMEM
TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                      TRANSMEM
TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                  TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db
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RECENTER FROWN N.A.

RECORDENCE FROWN N.A.

RECORDENCE FROWN N.A.

RECORDENCE FROWN N.A.

RECORDENCE S.B., Holt R.A., Evans C.A., Gocayne J.D.,

RAMAMER M.D., Celniker S.E., Holt R.W., Hoskins R.A., Galle R.E.,

RA Amanatides P.G., Scherer S.E., Holt R.W., Hoskins R.A., Galle R.E.,

RA Amanatides P.G., Scherer S.E., Holt R.W., Hoskins R.A., Henderson S.N.,

RA SURTON G.G., Wortenan J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej K.G., Change M., Pfeiffer B.D.,

RA Bril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basun A., Baxendale J., Bayraktaroglu L., Besaley B.M.,

RA Ballew R.M., Basun B.P., Blandari D., Bolshakov S.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Dunk P.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Dodson K., Doup L.E., Garg N.S., Gelbart W., Glaschmann M.,

RA Posler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.L., Harvey D., Heiman T.J., Wernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Heiman T.J., Wei m. H., Jobeyam C.,

RA Harris N.L., Lei Y., Levitsky A.A., Liu J., Lai Z., Liang Y., Lin X.,

Raksko P., Leit Y., Andlesh T.C., Kravitz S., Kulp D., Lai Z.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., Morberson D.L.,

Mount S.M., Moy M., Murphy B., Murphy L., Morshy D.M., Nelson D.L.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Morshy D.M., Nelson D.L.,
                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                            .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Haxapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                       63.9%; Score 39; DB 1; Length 360; 100.0%; Pred. No. 47; 0; Mismatches 0; Indels
                                                                                                                                                         EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                           -LINKED (GLCNAC. . .) (PC 9A7F70C982A632D1 CRC64;
                                                                                    EXTRACELLULAR (POTENTIAL)
                                                 CYTOPLASMIC (POTENTIAL).
                                                                                                                       (POTENTIAL)
                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable cytochrome P450 6t1 (RC 1.14.-.) (CYPVIT1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       529 AA
                                                                                                                                                                                                                                                                                  BY SIMILARITY.
                                                                                                                                                                                                            (POTENTIAL)
                                                                                                                       CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                        40625 MW;
                                                                                                                                                                                                                                                                                                                                                                         63.98;
                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                  316
119
10
24
360 AA;
                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               158 KWHWV 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYP6T1 OR CG1644.
                                                                                                                                                                                                                                                                                                                                                                                                                                             ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                             4 KWHWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C6T1 DROME
09VRI9;
Chemotaxis.
DOMAIN
                                                                    TRANSMEM
DOMAIN
                                                                                                                       DOMAIN
TRANSMEM
                                                                                                                                                                                              DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                   RANSMEM
                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                         RANSMEM
                                                                                                                                                                             FRANSMEM
                                                                                                                                                                                                                                                   FRANSMEM
                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                          DOMAIN
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                                                                                                                                                                                                                                                                    DOMAIN
                                                     DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Nature 397:176-180(1999).
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                  SO TWENTY WAY WAS A COURT OF THE COURT OF TH
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Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Ralazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
A Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Syler E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
A Syler E., Sanders E., Wang A.H., Wang X.,
Muliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
A Lhong K.H., Zhong F.N., Zhong W., Zhong G., Zhong J.,
A chong X.H., Zhong F.W., Zhong W., Zhong S., Zhu X., Smith H.O.,
C J., Yeh BREAKDOWN OF SYNTHETIC INSCRIDES (BY SIMILARITY).
C IN THE BREAKDOWN OF SYNTHETIC INSCRIDES (BY SIMILARITY).
C Oxidized Flavoprotein H.H.(2)O.
C Oxidized Flavoprotein H.H.(2)O.
C Oxidized Flavoprotein H.H.(2)O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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HSSP; P14779; 1.172.
HSSP; P14779; 1.172.
HSSP; P14779; 1.172.
HSSP; P14779; 1.172.
F17828: F290031182; Cyp6t1.
PRINTS; PRO0085; P450; 1.
PROSITE; PS00086; CYTOCHROME P450; 1.
Oxidoreductase; Monooxygenase; Membrane; Heme; Microsome;
Bridoplasmic reticulum; Hypothetical procein.
Bridoplasmic reticulum; Hypothetical procein.
BRIDAL
H72 472
H72 H72
H72 H72
SEQUENCE 529 AA; 60518 MW; 2BAD7875F3BD9C10 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown B.D., Doig P.C., Smith D.R., Noonan B., Guild B.C., deJonge B.L., Garmel G., Tummino P.J., Carus G., Uria-Nickelsen M., Mills D.M., Ives C., Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genomic sequence comparison of two unrelated isolates of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum
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16-OCT-2001 (Rel. 40, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Sec-independent protein translocase protein tatA/E homolog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63.9%; Score 39; DB 1; Length 529; 83.3%; Pred. No. 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: Belongs to the cytochrome P450 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99120557; PubMed=9923682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83.3%;
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Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 LHKWHW 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TATA HELPJ
09ZMB8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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TATA_HELPJ
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0
-!- FÜNCTION: REQUIRED FOR CORRECT LOCALIZATION OF PRECURSOR PROTEINS
BEARING SIGNAL PEPTIDES WITH THE TWIN ARGININE CONSERVED MOTIF
S/T-R-R-X-F-L-K. THIS SEC-INDEPENDENT PATHWAY IS TERMED TAT FOR
TWIN-ARGININE TRANSLOCATION SYSTEM. THIS SYSTEM MAINLY TRANSPORTS
PROTEINS WITH BOUND COFACTORS THAT REQUIRE FOLDING PRIOR TO EXPORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pylori."7

Nature 388:539-547 (1997).

Nature 388:539-547 (1997).

PERRING SIGNAL PEPTIDES WITH THE TWIN ARGININE CONSERVED MOTIF
S/T-R-R-X-F-L-K. THIS SEC-INDEPENDENT PATHWAY IS TERRED TAT FOR
TWIN-ARGININE TRANSLOCATION SYSTEM THIS SYSTEM MAINLY TRANSPORTS
PROTEINS WITH BOUND COPACTORS THAT REQUIRE FOLDING PRIOR TO EXPORT
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Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Tomb J.-F., White O., Kerlavage A.R., Klenk H.-P., Gill S., Dougherty B.A.,
Pleischmann R.D., Ketchum K.A., Xlenk H.-P., Gill S., Dougherty B.A.,
Nolson K., Quackenbuch J., Zahou L., Kirkness B.F., Peterson S.,
Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,
Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
Cotton M.D., Weidman J.M., Pujii C., Bowman C., Watthey L., Wallin B.,
Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria, Proteobacteria, Epsilonproteobacteria, Campylobacterales,
Helicobacteraceae, Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complete genome sequence of the gastric pathogen Helicobacter
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PIR; A71948, A71948.
HAMAP; MF.00236; -.
InterPro; IPR003369; MttA. Hcf106.
InterPro; IPR005312; TatA.E.
Pfam; PF02416; MttA. Hcf106; 1.
TIGRPAM; TIGROHII; tatA.E.
Transport; Protein transport; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
18-SPER-2003 (Rel. 41, Last annotation update)
Sec-independent protein translocase protein tatA/E homolog.
TATA OR HP0320.
                                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION: Inner-membrane bound (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79 AA; 8752 MW; D39E9DCA02AA5E8F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62.3%; Score 38; DB 1; 55.6%; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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STRAIN=26695 / ATCC 700392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 FLHKWHWVV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TATA HELPY
O25088;
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17085 MW; 0AD6F21157060A4C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G -> A (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
31;
-!- SUBUNIT: Homodimer.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO THE UPF0098 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
SCO1794 OR SCIS.02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62.3%; Score 38; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ecodene; Ed11238; ybhB.
LinterPro; IPR001247; Cons_hypoth481.
InterPro; IPR001858; PBP.
Pfam; PF01161; PBP; 1.
TICRPAMS; TIGR00481; TIGR00481; 1.
3D-structure; Complete proteome.
CONFLICT 136 136 G -> A (I
                                                                                                                                                                                                                                                                                                                                                                           EMBL, AE000180, AAC73860.1; -. PIR, E64813, Q3ECBA.
PDB; 1FJJ; 18-JUL-01.
                                                                                                                                                                                                                                                                                                                                             EMBL; J04423; AAA23513.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136
147
158 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 WHWVV 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 WHWVV 9
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STRAND
SEQUENCE
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YH94 STRCO
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                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDILINE=89066784; PubMed=3058702;
MEDILINE=89066784; PubMed=3058702;
Octsuka A.J., Buoncristiani M.R., Howard P.K., Flamm J., Johnson O., Yamamoto R., Uchida K., Cook C., Ruppert J., Matsuzaki J.;
"The Bscherichia coli biotin biosynthetic enzyme sequences predicted from the nucleodide sequence of the bio operon.";
J. Biol. Chem. 263:19577-19585 (1988).
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Serre L., Pereira de Jesus K., Zelwer C., Bureaud N., Schoentgen F.,
Benedetti H.;
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SERAIN=K12 / WG1655.
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Crystal structures of YBHB and YBCL from Escherichia coli, two bacterial homologues to a Raf kinase inhibitor protein."; J. Mol. Biol. 310:617-634(2001).
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                                                                                                                                                                                                                                                                                                                                                                     PIR; H64559; H64559.

TIGR; HP03020; --
HAMAP; MF 00236; --; 1.

InterPro; IPR005312; TatA_E.

Pfam; PF02416; MttA_Hcf106.

ITIGRFAMs; TIGR011; tatA_E.

TIGRFAMs; TIGR011; tatA_E:

TIGRFAMs; TIGR011; tatA_E:

Transport; Protein transport; Transhembrane;
                          SUBCELLULAR LOCATION: Inner-membrane bound (Probable). SIMILARITY: BELONGS TO THE TATA/E FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose
Mau B., Shao Y.,
"The complete genome sequence of Escherichia coli K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 38; DB 1; Length 79;
Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
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CES99ACA02AA5E8F CRC64;
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01-JAN-1990 (Rel. 13, Created)
N-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         158 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        membrane; Complete proteome
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NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                             EMBL; AE000550; AAD07397.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79 AA; 8722 MW;
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Best Local Similarity 55.v.,
5; Conservative
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        SIMILARITY)
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258 2
380 AA;
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P53053;
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TRANSMEM
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COSC_YEAST
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                                              MEDLINE-21996410; PubMed=12000953;
MEDLINE-21996410; PubMed=12000953;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Olveil S.,
Rabbinowitsch E., Rajandram M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness B.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutron G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.K., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoglagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                              "Complete genome sequence of the model actinomycete Streptomyces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria, Proteobacteria, Gammaproteobacteria, Pasteurellales,
Pasteurellaceae, Haemophilus.
NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             TICRFAMS; TIGR00481; TIGR00481; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 179 AA; 19158 MW; AC4A6A43BD830861 CRC64;
 Streptomycineae; Streptomycetaceae; Streptomyces,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62.3%; Score 38; DB 1;
100.0%; Pred. No. 34;
ive 0; Mismatches
                                                                                                                                                                                                          coelicolor A3(2).";
Nature 417:141-147(2002).
-!- SIMILARITY: BELONGS TO THE UPF0098 FAMILY.
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(Rel. 32, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              367 AA
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PIR, T36855, T36855.
HSSP, P77368; IFUX.
INTERPRO, IPRO05247; CONS_hypoth481.
InterPro; IPRO01858; PBP.
Pfam; PF01161; PBP; 1.
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STRAIN-Rd / KW20 / ATCC 51907;
MEDLINE-95350630; PubMed-754280.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein HI1236.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                   Hopwood D.A.;
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01-NOV-1995
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YC36_HAEIN
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"Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.";
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Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes, Saccharomycetales, Saccharomycetales, Saccharomycetales, Saccharomycetales, Saccharomyces.
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-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: BELONGS TO THE DUP/COS FAMILY.
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STRAINS=S288c / FY1679;
MEDLINE=97127827; PubMed=8972578;
Coissac E., Maillier E., Robineau S., Netter P.;
"Sequence of a 39,411 bp DNA fragment covering the left end of chromosome VII of Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62.3%; Score 38; DB 1; Length 367;
80.0%; Pred. No. 67;
ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGR; H11236; -. mr. Transmembrane; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             367 AA; 41355 MW; B00211C5F98C2585 CRC64;
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52F58F4E400CA596 CRC64;
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01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
                                                                 Science 269:496-512(1995).
-!- SIMILARITY: TO E.COLI YDGA AND YIHF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
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Transmembrane; Multigene family
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U32803; AAC22888.1; -. PIR; F64022; F64022.
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COS12 OR YGL263W OR NRC380.
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MEDLINE=205643103; PubMed=10961996;
MEDLINE=205643103; PubMed=10961996;
Voir R., Feldmaier-Fuchs G., Schweikardt T., Decker H., Burmester T.;
"Complete sequence of the 24-mer hemocyanin of the tarantula Burypelma californicum. Structure and intramolecular evolution of the
                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Biol. Chem. 275:39339-39344 (2000).
-!- FUNCTION: HEMOCYANINS ARE COPPER-CONTAINING OXYGEN CARRIERS
OCCURRING FREELY DISSOLVED IN THE HEMOLYMPH OF MANY MOLLUSKS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ARTHROPODS.
-!-SUBUNIT: TARANTULA HEMOCYANIN IS A 24-CHAIN POLYMER WITH SEVEN DIFFERENT CHAINS IDENTIFIED.
-!-SUBCELLULAR LOCATION: Extracellular.
-!-TISSUE SPECIFICITY: Hemolymph.
-!-TISSUE SPECIFICITY: Hemolymph.
-!-LIGANDS (PRESUMABLY CONPER IONS BOUND EACH HAVE 3 NITROGEN LIGANDS (PRESUMABLY CONTRIBUTED BY HIS RESIDUES) AND SHARE A BRIDGING LIGAND (POSSIBLY CONTRIBUTED BY A TYR RESIDUE) IN ADDITION TO BINDING OXYGEN.
-!-SIMILARITY: BELONGS TO THE TYROSINASE FAMILY. HEMOCYANIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eurypelma californica (American tarantula).
Eukaryota, Metazoa, Arthropoda, Chelicerata, Arachnida, Araneae,
Mygalomorphae, Theraphosidae, Aphonopelma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "COpper; Glycoprotein; Hemolymph.
BY SIMILARITY.
BY SIMILARITY.
COPPER 1 (BY SIMILARITY).
COPPER 1 (BY SIMILARITY).
COPPER 1 (BY SIMILARITY).
COPPER 2 (BY SIMILARITY).
COPPER 2 (BY SIMILARITY).
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      DB 1; Length 380;
                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Score 38; DB 1
Pred. No. 69;
1; Mismatches
                                                                                                                                                                                                                                                                                                               628 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EWBL; AJ277489; CAB89495.1; --
HSSP; P04253; 1LLA.
Interpro; IPR000896; Hemocyanin.
Interpro; IPR005203; hemocyanin.C.
Interpro; IPR005204; hemocyanin.N.
Interpro; IPR00227; Tyrosinase.Pfam; PF00372; hemocyanin; 1.
Pfam; PF03723; hemocyanin; 1.
PR031TE; PS00209; HEMOCYANIN.C; 1.
PROSITE; PS00210; HEMOCYANIN.Z; 1.
PROSITE; PS00210; HEMOCYANIN.Z; 1.
PROSITE; PS00498; TYROSINASE_Z; 1.
   62.3%;
80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hemocyanin C chain (HcC).
                                                            4; Conservative
                                                                                                                                                                                                                                                                                                               STANDARD;
      Query Match
Best Local Similarity
                                                                                                                                                                     194 KWHWI 198
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INIT_MET 0
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                                                                                                                  4 KWHWV 8
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178
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28-FEB-2003
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METAL
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HCYC EURCA

HCYC EURCA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=91025623; PubMed=2222854; MEDLINE=91025623; PubMed=2222854; Schartau W., Metzger W., Sonner P., Geisert H., Storz H.; Schartau W., metzger W., Sonner P., Geisert H., Storz H.; Schartau W., metzger W., Sonner P., Geisert H., Storz H.; Subunit a of Eurypelma californicum hemcoyanin."; Biol. Chem. Hoppe-Seyler 371:557-565(1990).
-i- FUNCTION: HEMCCYANINS ARE COPPER-CONTAINING OXYGEN CARRIERS OCCURRING FREELY DISSOLVED IN THE HEMOLYMPH OF MANY MOLLUSKS AND
                                                                                                                                                                                                                                 Gaps
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-I-SUBUNIT: TARANTULA HEMOCYANIN IS A 24-CHAIN POLYMER WITH SEVEN
DIFFERENT CHAINS IDENTIFIED.
-I-SUBCELLULAR LOCATION: Extracellular.
-I-SUBSUE SPECIFICITY: Hemolymph.
-I-MISCELLANBOUS: THE TWO COPPER IONS BOUND EACH HAVE 3 NITROGEN
LIGANDS (PRESUMABLY CONTRIBUTED BY HIS RESIDUES) AND SHARE A
BRIDGING LIGAND (POSSIBLY CONTRIBUTED BY A TYR RESIDUE) IN
ADDITION TO BINDING OXYGEN.
-I-SIMILARITY: BELONGS TO THE TYROSINASE FAMILY. HEMOCYANIN
SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SECUENCE FROM N.A.
MEDLINE=91060544; PubMed=2246235;
WIDDLINE=91060544; PubMed=2246235;
Wort R., Feldmaider-Fuchs G.;
"Arthropod hemocyanine. Molecular cloning and sequencing of cDNAs encoding the tarantula hemocyanin subunits a and e.";
J. Biol. Chem. 265:19447-19452 (1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Burypelma californica (American tarantula).
Eukaryota, Metazoa, Arthropoda; Chelicerata; Arachnida; Araneae;
Mygalomorphae; Theraphosidae; Aphonopelma.
NCBI_TaxID=29932;
COPPER 2 (BY SIMILARITY).

N-LINKED (GLCNAC. .) (POTENTIAL)

N-LINKED (GLCNAC. ..) (POTENTIAL)

EC2F8ED04935DFBD CRC64;
                                                                                                                                                                                                                                 .
0
                                                                                                                                                                   Length 628;
                                                                                                                                                                Score 38; DB 1; Length 628
Pred. No. 1.1e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-APR-1990 (Rel. 14, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hemocyanin A chain (HcA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               630 AA.
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InterPro; IPR005203; Hemocyanin_C.
InterPro; IPR005204; Hemocyanin_N.
InterPro; IPR00227; Tyrosinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00372; hemocyanin; 1.
Pfam; PF0372; hemocyanin C; 1.
Pfam; PF03722; hemocyanin N; 1.
PRINTS; PR00187; HAEMOCYANIN.
                                                                                               72435 MW;
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                                                                                                                                                                similarity 71.4%;
5, Conservative
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      365
450
617
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   365 3
450 4
617 6
628 AA;
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Best Local Similarity
Matches 5; Conserv
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      METAL
CARBOHYD
CARBOHYD
                                                                                                  SEQUENCE
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HCYA_EURCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDINE=95350630; PubMed=7542800;

Pleisdofmann R.D., Adams M.D., White O., Clayton R.A., Kirkness B.F.,

Rerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kellay J.M.,

Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoglagen N.S.M.,

Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    White O., Clayton R.A., Kerlavage A.R., Fleischmann R.D., Peterson Harkey E., Dodson R., Gwinn M.; Submitted (MAY-1998) to the FMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                      COPPER 1 (PROBABLE).
COPPER 1 (PROBABLE).
COPPER 2 (PROBABLE).
COPPER 2 (PROBABLE).
COPPER 2 (PROBABLE).
SOPPER 2 (PROBABLE).
BY SIMILARITY.
N-LINKED (GLCNAC. . ) (POTENTIAL).
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Pasteurellaceae, Haemophilus.
NCBI_TaxID=727;
                                                                             transport; Copper; Glycoprotein; Hemolymph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 38; DB 1; Length 630
Pred. No. 1.18+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       4F6989963C1CC793 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 39, Created)
(Rel. 39, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  138 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
HEMOCYANIN 1; 1.
HEMOCYANIN 2; 1.
TYROSINASE 2; 1.
                                                                                                                174 174
178 178
205 205
29 329
39 365
3 365
3 466 N
450 N
72187 MW;
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71.4%;
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Query Match
Best Local Similarity 71.4°,
Best Si Conservative
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                                                                                                                                                                                                                                                                                                                                                                                              620
630 AA;
                        PROSITE; PS00210; H
PROSITE; PS00498; T
Transport; Oxygen t:
INIT MET 174
METAL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 НКМНМVV 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
TB27 HABIN
AC 086234
DT 30-MAY-2000
DT 30-MAY-2000
DT 30-MAY-2000
DT 28-FEB-2003
DE HYPOTHETICAL
GN HIRLST
CC BACTERIA, PY
CC PASTERIALS PY
CC CASTRAIN-RG /
RN HILLST
RN (1)

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28-FEB-2003
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DISULFID
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     PROSITE;
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Gaps
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                                                                 Score 37; DB 1; Length 138;
Pred. No. 38;
1; Mismatches 0; Indels
Hypothetical protein; Transmembrane; Complete proteome.
TRANSMEM 12 32 POTENTIAL.
                                              8833E1195A6184EC CRC64;
                                                                                                                                                                          December 16, 2003, 14:15:15
                         POTENTIAL.
                                    POTENTIAL
                                    131 P
15598 MW;
                                                                     60.7%;
                                                                               Local Similarity 83.3
                12
62
111
138 AA;
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109 HKFHWV 114
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Job time : 6.66667 secs
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                                               SEQUENCE
                         TRANSMEM
                                    TRANSMEM
                                                                      Query Match
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anopheles g anopheles g

drosophila drosophila

galleria me

drosophila drosophila

anopheles g armigeres s holotrichia

aedes aegyp tenebrio mo anopheles g aedes aegyp bombyx mori

holotrichia manduca sex

095143 09W1V6 076951 076951 09V551 09V5752 09V5731 09G7W1 09G747 09G7W2 09G7W2 09G7W3 09G7W3

Sequence:

Run on:

Searched:

Database

aedes aegyp anopheles g anopheles g anopheles s anopheles g

bombyx mori

sarcophaga

anopheles g

Q9gva6 Q25519 Q8mzm4 Q76208 09gva5

hyphantria

pimpla hypo

pimpla hypo manduca sex

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SEQUENCE FROM N.A.

STRAIN-ATCC 19089 / CR15;

STRAIN-ATCC 19089 / CR15;

MEDLINE-2117-9698; PubMed=11259647;

Micrman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

Bisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,

Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,

Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;

"Complete genome sequence of Caulobacter crescentus.";

Proc. Natl. Acad. Sci. US.A. 98:4136-4141(2001).
                                                                                                                                                                                                                                                                                                                            Caulobacter crescentus.
Bacteria, proteobacteria, Alphaproteobacteria, Caulobacterales, Cayrobacteracese, Cayrobacter. Gaulobacter.
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                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (FrEMBLrel. 20, Last annotation update)
Hypothetical protein CC3059.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 46; DB 16;
Pred. No. 12;
2; Mismatches 0
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                                                         0967WI
097047
096751
09816K2
0816K2
0816K1
084249
084249
0967W2
0967W2
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044251
096453
096753
09GVA6
Q25519
Q8MZM4
       Q95R43
Q9W1V6
Q964D5
                              076951
Q811F6
096752
Q9V521
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5, Conservative 2
 PRELIMINARY
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LHQWHWI 23
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Best Local Similarity
Matches 5; Conserv
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Hypothetical
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Q9A3Z1
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OBP739 xanthomonas
OBP70 xylella fas
O92r87 zinnia eleg
O8rw89 rhizobium 1
Q8rhf3 fusobacteri
O8e814 shewanella
Q8xx91 pyrobaculum
Q8mp4 caenorhabdi
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Q8peh7 xanthomonas
Q92wul rhizobium m
Q9bld9 drosophila
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29xmg3 epichloe ty
28kgt4 xanthomonas
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                                                  December 16, 2003, 14:09:45; Search time 25 Seconds (without alignments) 92.899 Million cell updates/sec
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                                                                                                                                                   830525
      GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                    830525 segs, 258052604 residues
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                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                    - protein search, using sw model
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Q8MPP4
Q9XMG3
Q8KQT4
Q8P338
Q8PBH7
Q9EH7
                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9A3Z1
Q8P1F4
Q8P739
Q9PFR0
Q9ZR87
Q8VM89
Q8RHF3
                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                         sp archa: *
sp archa: *
sp bacteria: *
sp fung: *
sp human: *
sp mammal: *
sp mto: *
sp phage: *
sp phage: *
sp phage: *
sp phage: *
                                                                                                                                                                                                                                                                                                                            unclassified:*
                                                                                                                                                                                                                                                                                                    sp_rodent:*
sp_virus:*
sp_vertebrate:*
                                                                                                                                                                                                                                                                                                                                   sp_rvirus:*
sp_bacteriap:*
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Maximum DB seq length: 2000000000
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16
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              Copyright
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Match
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Perfect score:
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209 AA.

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Gaps

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; 0

Length 209; Indels

Result Š.

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STRAIN=9a5c;
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셤
                                                                                                                                                                                                                                                                                                                                           RC STRAINS 16 / ATCC 13902 / XV 101;

RA da Silva A.C. R. Perro J.A. Reinach F.C., Farah C.S., Furlan L.R.,

RA da Silva A.C. R., Perro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

RA Alves L.M.C., do Amaral A.M., Bertolnin M.C., Camargo L.B.A.,

RA Alves L.M.C. do Amaral A.M., Bertolnin M.C., Camargo L.B.A.,

RA Camarotte G., Cannavan P., Carboro J., Chambergo F., Ciapina L.P.,

RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos B.G.M., Lemos M., Lemos M., Cannavan B.D., Martins E.C., Machado M.A., Madeira A.M., Miyaki C.Y., Moon D.H.,

RA Martins E.C., Machado M.J., Madeira A.M. B.N., Miyaki C.Y., Moon D.H.,

RA Martins E.C., Machado M.J., Noura V.K., Oliveira W.C., Oliveira V.R.,

RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,

RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

ROMPATISON Of the genomes of two Xanthomonas pathogens with differing T. Nous specificities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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STRAIN=ATCC 33913 / NCPPB 528;
MEDLINE=22022145; PubMed=12024217;
MEDLINE=22022145; PubMed=12024217;
Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
Alves L.M.C., do Amaral A.M., Bertollini M.C., Camargo L.E.A.,
Camarotte G., Cannavan F., Cardozo J., Chambergo F., Clapina L.P.,
Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xanthomonas campestris (pv. campestris).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
                                                                                                                                                                                                                               Xanthomonas axonopodis (pv. citri).
Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales,
Xanthomonadaceae, Xanthomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 protein; Complete proteome.
213 AA; 23920 MW; 900172C92CE7B10C CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                           01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein XAC2944.
                                                                  213 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE011936; AAM37789.1; -.
InterPro; IPR005797; Cytb_b6_N.
PROSITE; PS00192; CYTOCHROME_B_HEME; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein XCC2775.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 417:459-463(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                      NCBI_TaxID=92829;
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                                                                                                                                                                                                              XAC2944.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8P739
Q8P739;
                                                                  Q8PIF4
Q8PIF4;
                      RESULT 2
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MEDLINES-2016-07.17; Purchae P., Arruda P., Abreu F.A., Acencio M., Alwaeranga R., Alves L.M.C., Arruda P., Abreu F.A., Acencio M., Alwaeranga R., Alves L.M.C., Arraya J.E., Baia G.S., Baptista C.S., Alwarenga R., Alves L.M.C., Arraya J.E., Bove J.M., Briones M.R.S., Buenco M.R.P., Camarco A.A., Carraro D.M., Carrer H., Camarco A.A., Camargo D.E.A., Carraro D.M., Carrer H., Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M., Action C. L.L., Cristofani M., Dias.Neto B., Doocean C., El-Dorry H., Farga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R., Farga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R., Anness B.E., Langer B.L., Kitajima J.P., Rrieger J.E., Kitajima J.P., Rrieger J.E., Hoheisel J.D., Junqueitra M.L., Kemper E.L., Kitajima J.P., Rrieger J.E., Hoheisel J.D., Junqueitra M.L., Kemper E.L., Kitajima J.P., Rrieger J.E., Madeira M.B.N., Madeira M.R., Machado J.A., Mandeira A.M.B.N., Madeira H.M.F., Matsukuma A.Y., Marchins B.A.L., Martins E.M.F., Matsukuma A.Y., Mandeira M.B., Madeira A.M.B.N., Madeira M.R., Matsukuma A.Y., Nobrega F.G., Miyaki C.Y., Montetro J.B.S., Mani A.Jr., Nobrega F.G., Miyaki C.Y., Montetro J.B.S., Abani A.Jr., Nobrega F.G., Muses L.R., Oliveira M.A., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B., Roberto P.G., Santelli R.V., Sawasaki H.E., Quaggio R.B., Roberto P.G., Santelli R.V., Sawasaki H.E., A silve A.C.R., da Silva A.M., M.L.Z., Siqueira W.J., Tsuhako M.H., A sago M.A., Tsuhako M.H., A sago M.A., Zatz M., Meidanis J., Setubal J.C., Tsuhako M.H., Sago M.A., Zatz M., Meidanis J., Setubal J.C., Inter G. Inter G
Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

Formighieri B.F., Franco M.C., Greggio C.C., Gruber A.,

Katsuyama A.M., Kishi L.T., Leite R.P., Lemos B.G.M., Lemos M.V.F.,

Locali B.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

Martins B.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

Spinola L.A.F., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D.,

Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

"Comparison of the genomes of two Xanthomonas pathogens with differing

Nature 417.459-463 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Xanthomonadaceae; Xylella.
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0
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Pred. No. 12;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein; Complete proteome.
SEQUENCE 214 AA; 23740 MM; 0F7BFDCC76937150 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE, PS00192; CYTOCHROME B HEME; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last seq
01-WAR-2002 (TrEMBLrel. 20, Last ann
Hypothetical protein Xf0597.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20365717; PubMed=10910347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterProj IPR005797; Cytb_b6 N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75.4%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE012390; AAM42047.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xylella fastidiosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 LHKWHWV 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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01-JUN-2002 (TrEMBLrel. 21,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shewanella oneidensis.
                                                                                                                                       124 LDKWHWVV 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                146 LDKWHWVL 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 LHKWHWVV 9
                                                                                                                2 LHKWHWVV 9
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                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                              NCBI_TaxID=76856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=70863;
                                                                                                                                                                                                                                                                                                      Fusobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QBEBL4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8E8L4
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MEDIJNE=20098724; PubMed=10631260;
Percez-Amador M.A., Abler M.L., De Rocher E.J., Thompson D.M.,
Percez-Amador M.A., Abler M.L., Ders A., Green P.J.;
"Identification of BFN1, a bifunctional nuclease induced during leaf
and stem senescence in arabidopsis.";
Plant Physiol. 122:169-179(2000).
EMBL; U90266; AAD00695.1; -.
HSSP; P24289; LAKO.
                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hosie A.H.F., Poole P.S.;
"Identification and characterisation of a novel monocarboxylic acid transporter of Rhizobium leguminosarum "; submitted (DEC-2001) to the BMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; campanulids; Asterales; Asteraceae; Asteroideae;
                                                                    o;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rhizobium leguminosarum (biovar viciae).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75.4%; Score 46; DB 10; Length 328; 71.4%; Pred. No. 18; 0; Indels ive 2; Mismatches 0; Indels
                                           75.4%; Score 46; DB 16; Length 218; 71.4%; Pred. No. 12; 1tive 2; Mismatches 0; Indels
EMBL; AE003905; AAF83407.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 218 AA; 24198 MW; A032E2AD602C24B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       328 AA; 37560 MW; 9343388936C53F7E CRC64;
                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        417 AA
                                                                                                                                                                          328 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                               Created)
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Interpro; IPR003154; S1/PInuclease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF02265; Nuclease; 1.
PROSITE; PS00190; CYTOCHROME C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2003 (TrEMBLrel. 23, mm.c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71.4%;
                                                                                                                                                                                              01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-MAX-2003 (TrEMBLrel. 23,
                                                         Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                               Bifunctional nuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Two-component sensor
                                                                                                                                                                                                                                                                                                     Heliantheae, Zinnia.
NCBI_TaxID=34245;
                                                                                                        ||:|||:
28 LHQWHWI 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ::|||||
75 WMHKWHW 81
                                                                                           2 LHKWHWV 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 FLHKWHW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=387;
                                                                                                                                                                                                                                                       Zinnia elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=3841;
                                                                                                                                                                                                          01-MAY-1999
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08VM89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8VM89
                                                                                                                                                                           Q9ZR87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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STRAIN=MR-1;
MEDDINE=22297686; PubMed=12368813;
Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
Read T.D., Eisen J.A., Seshadri E., Ward N., Methe B., Clayton R.A.,
Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S.,
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EMBL, AR01511; AAL94167.1;
                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                    2; Length 417;
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EMBL; AJ421944; CAD19126.1; -.
InterPro; IPR003594; ATPbind_ATPase.
Pffam; PF02518; HATPase_c; 1.
SMART; SM00387; HATPase_c; 1.
SEQUENCE 417 AA; 45820 MW; 2034030279B9E996 CRC64;
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SEQUENCE 196 AA; 23169 MW; 4438206B0BCCB0C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Hypothetical protein FN2083.
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75.4%; Score 46; DB
Best Local Similarity 87.5%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches
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MEDLINE=21886394; PubMed=11889109;
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
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                                                    SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
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01-NOV-1999 (TrEMBLrel. 12, Last
01-OCT-2002 (TrEMBLrel. 22, Last
Et2.OL ORP! protein (Fragment).
ET2.OL ORP!
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50.0%;
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Best Local Similarity 50.0.
Best A; Conservative
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5; Conservative
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94 FMHRFHWI 101
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     SEQUENCE FROM N.A.
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Mitochondrion.
                  Wallis J.M.;
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Best Local S
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Q8KQT4
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Rhabditidae; Peloderinae; Caenorhabditis.
DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Vamethevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C., Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., "Feldblyun T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M., "Genome sequence of the dissimilatory metal ion-reducing bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
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                                                                                                                                                                68.9%; Score 42; DB 16; Length 486; 62.5%; Pred. No. 1.1e+02; tive 3; Mismatches 0; Indels
                                                                         Shewanella oneidensis.";

Nat. Biotechnol. 20:1118-1123(2002).

EMBL, AE015886; AAN57609.1; -.

TIGR; SO4649; -.

Hypothetical protein; Complete proteome.

SEQUENCE 486 AA; 57471 MW; B25617A4A982564F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                    Archaea; Crenarchaecta; Thermoprotei; Thermoproteales;
Thermoproteaceae; Pyrobaculum.
NCBI TaxID=13773;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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Last annotation update)
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EMBL, AE009814; AAL63387.1; -.
InterPro, IPR000914; SBP bac_5.
Pfam; PF00499; SBP_bac_5; 3.
Complete proteome.
SEQUENCE 737 AA; 82378 MW; BCFC9D3E46354725
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STRAIN-IM2 / AICC 51768 / DSM 7523;
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01-0CT-2002 (TrEMBLrel. 22,
01-0CT-2002 (TrEMBLrel. 22,
Y46G5A.33 protein.
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Best Local Similarity 62..
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Best Local Similarity 62.5
Matches 5; Conservative
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Q8MPP4
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MDDLINEPRG;
MOGEN K.L., Siegel M.R., Schardl C.L.;
Mogen K.L., Siegel M.R., Schardl C.L.;
Mogen K.L., Siegel M.R., Schardl C.L.;
"Linear DNA plasmids of the perennial ryegrass choke pathogen Epichloe typhina (Clavicipitaceae).";
Curr. Genet. 20:519-528(1991).
ENBL; X57200; CAA40486.2;
InterPro; IPRO00477; RVTse.
InterPro; IPRO0078; rvt; 1.
ENBL directed DNA polymerase; Transferase; Mitochondrion; Plasmid.
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Xanthomonas campestris (pv. campestris).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
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Hypocreales; Clavicipitaceae; Epichloe.
NCBI_TaxID=5113;
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"Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                     Score 41; DB 5; Length 145;
Pred. No. 47;
4; Mismatches 0; Indels
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                      investigating biology.";
Science 282:2012-2018(1998).
EMBL, AL110485; CAD36500.1; -
SEQUENCE 145 AA, 16489 MW; 50B4B1F300F7D357 CRC64;
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Last sequence update)
Last annotation update)
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NCBI_TaxID=92829;
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SEQUENCE FROM N.A.

SEQUENCE 23913 / NCPPB 528;

MEDINE=22022145; PubMed=12024217;

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                                                                            SEQUENCE FROM N.A.

WEDLINE=22034956; PubMed=12039751;

WEDLINE=22034956; PubMed=12039751;

Yen M.R., Lin N.T., Hung C.H., Choy K.T., Weng S.F., Tseng Y.H.;

"oriC Region and Replication Termination Site, dif, of the Xanthomonas
campestris pv. campestris 17 Chromosome.";

Appl. Environ. Microbiol. 68:2924-2933(2002).

EMBL; AY057934; AAL30086.1; --

EMBL; AX057934; AAL30086.1; --

EMBL; PF02096; 60KD IMP; 1-

PERINTS; PRO0701; 60KDINNERMP.
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Xanthomonadaceae, Xanthomonas.
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Pred. No. 1.8e+02;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          67.2%; Score 41; DB 2; Length 573; 55.6%; Pred. No. 1.8e+02; tive 1; Mismatches 3; Indels
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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EMBL; ABC12552; AAW43456.1; -.
InterPro; IPR001708; 60kDa_innermeb.
Pfam; PF02096; 60KD IMP; 1.
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Xanthomonadaceae; Xanthomonas.
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PRINTS; PR00701; 60KDINNERMP.
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55.6%;
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Best Local Similarity 55.00,
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                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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SEQUENCE FROM N.A.

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MEDINRE-2020145; PubMed-12024217;

A BALVE A.C.R.; Ferro J.A.; Reinach F.C.; Farah C.S.; Furlan L.R.;

A Canaggio R.B.; Monteiro-vitorello C.B.; Van Sluys M.A.; Almeida N.F.;

A Alves L.M.C.; do Amaral A.M.; Bertolini M.C.; Camargo L.B.A.;

A Camarotte G.; Cannavan F.; Cardozo J.; Chambergo F.; Ciapina L.P.;

A Camarotte G.; Cannavan F.; Cardozo J.; Chambergo F.; Ciapina L.P.;

R Aria J.B.; Ferreira A.G.S.; Ferreira R.C.C.; Ferro M.I.T.;

R Aria J.B.; Ferreira A.G.S.; Ferreira R.C.C.; Ferro M.I.T.;

R Aria J.B.; Mishi L.T.; Leite R.P.; Lemos B.G.M.; Lemos M.V.F.;

R Aria J.B.; Meddon M.A.; Madaira A.M.B.; Martinez-Rossi N.M.;

Moreira L.M.; Royo M.T.M.; Okura V.K.; Oliveira M.C.; Oliveira V.R.;

Pereira L.M.; Royo M.T.M.; Okura V.K.; Oliveira M.C.; Oliveira V.R.;

Pereira L.M.; Rossi A.; Sena J.A.D.; Silva C.; de Souza R.F.;

Setubal J.C.; Kitajima J.P.;

Trindade dos Santos M.; Truffi D.; Tsai S.M.; White F.F.;

Setubal J.C.; Kitajima J.P.;

"Comparison of the genomes of two Xanthomonas pathogens with differing Rather 417459-463 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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MEDLINE=21396508; PubMed=11481431;
Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P.,
Vorhoelter F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J.,
                                                                                                                                                                                                                                                   Xanthomonas axonopodis (pv. citri).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ·.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Sinorhizobium.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein RB0238.
RB0238 OR SMB20248.
Rhizobium meliloti (Sinorhizobium meliloti).
                                                           01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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PRINTS; PR00701; 60KDINNERMP.
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PRELIMINARY;
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Best Local Similarity
Matches 5; Conserv
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SEQUENCE 574 AA;
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RA Golding B., Puehler A.;

RT "The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-
RT fixing endosymbiont Sinchizobium mellioti.";

RL Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).

DR EMBL; AL603642; CAC48638.1; -.

KW Plasmid; Hypothetical protein; Complete proteome.

SQ SEQUENCE 582 AA; 63374 MW; 2E20B800DB09B2B CRC64;

Query Match

Best Local Similarity 62.5%; Pred. No. 1.8e+02;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LHKWHWVV 9

463 LHKWHWVV 470
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Search completed: December 16, 2003, 14:18:00 Job time : 26 secs

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(GENZ ) GENZYME CORP
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Synthetic.
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Human cancer antig
Novel human secret
Drosophila melanog
Human novel protei
Drosophila melanog
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Bombyx mori (pro)p
Prophenol oxidase.
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                                                                                                         December 16, 2003, 14:06:05; Search time 33 Seconds (without alignments) 43.289 Million cell updates/sec
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| SIDSI/gcgdata/geneseqp-embl/AA1980.DAT:*
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| SIDSI/gcgdata/geneseqp-embl/AA1981.DAT:*
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                                                                                                                                                                                                                                                                                                                                                             1107863
5.1.6
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                       1107863 segs, 158726573 residues
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GenCore version (c) 1993 - 2003
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Maximum Match 100%
Listing first 45 summaries
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AAU31978
ABB57797
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ABB57998
AAR89115
AAW14441
                                                                         sw model
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                                                                         protein search, using
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64
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Match 1
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7 4 4 4 4 4 4
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Maximum DB
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                    Streptococcus poly
Novel human diagno
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      Staphylococcus aur
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                                                                                                                                                                                                                                                                                                                                                       lumapf, cancer antigen; ATF4; CREB-2; vaccine; cytostatic;
impunogenic ligand; gene therapy; WHC; major histocompatibility complex;
Adoptive immunotherapy; cancer; ovarian cancer.
                                        Sequence of novel
                                                                                                                                                                                                                                                                                                                                         Human capeer antigen ATF4/CREB-2 based immunogenic ligand #4.
                                                                                                                                                                                                                                                                ALICAMENTS
                                                                   AAY07385
AAY99606
ABP60489
ABP60490
ABP60491
AAW08195
AAW08195
AAW08195
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AAR31363
AAR34288
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AAW14499
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AAR10578
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ABP26523
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AAR25434
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30-MAY-2001; 2001WO-US17454.
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20-DEC-2000; 2000US-257007P.
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whose sequence is based in part on residues 42-50 of human cancer antigen ATF4/CREB-2 (not defined) and the polynucleotides encoding them. Also included are an antibody that specifically recognises and binds the compound, a method for inducing an immune response in a subject by delivering the compound, a method of immunotherapy comprising limbs the campound, a method of immunotherapy comprising that has delivering the compound, a method of immunotherapy comprising limbs the campoint to a subject the antibody, an immune effector cell that has been raised in vitro or in vivo in the presence and at the expense of an antigen presenting cell that presents the immunogenic compound in the context of an MFC (major histocompatibility complex) molecule and a method of adoptive immunotherapy comprising administering the immune response effector cell. The compounds are useful for modulating an immune response context of an antirally occurring compounds are especially useful in gene therapy or as components of anti-cancer vaccines. The compounds are useful for treating cancer, particularly covarian cancer. The compounds are also useful for generating antibodies that specifically recognise and bind to these molecules. These campoinds are larged to a subject. The peptides, polypeptides and polynucleotides are useful in diagnostic methods, for the detection and purification of antibodies; or as immunogen for the production of antibodies. The present immunogenic methods a human cancer antigen ATF4/CREB-2 based immunogenic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; cancer antigen; ATF4; CREB-2; vaccine; cytostatic; immunogenic ligand; gene therapy; MHC; major histocompatibility complex; adoptive immunotherapy; cancer; ovarian cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          respectively
New therapeutic compounds comprising immunogenic ligands, useful for modulating an immune response, particularly for treating ovarian cancer, and as components of anticancer vaccines
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               but have not been cross-referenced or CDS features put in due to the degeneracy of the DNA sequences.
                                                                                                                             The invention relates to compounds comprising an immunogenic ligand
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human cancer antigen ATF4/CRBB-2 based immunogenic ligand #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ilarity 100.0%; Score 64; DB 23; Length 9; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Note: Immunogenic ligands AAU74681-AAU74686 are stated to encoded by the degenerate DNA sequences AAS20120-AAS20125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU74683 standard; Peptide; 9 AA.
                                                                                      Claim 4; Page 56; 68pp; English
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20-DEC-2000; 2000US-257007P.
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Best Local Similarity
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The invention relates to compounds comprising an immunogenic ligand whose sequence is based in part on residues 42-50 of human cancer antigen ATF4(TREB-2 (not defined) and the polymuclectides encoding them. Also included are an antibody that specifically recognises and binds the compound, a method for inducing an immune response in a subject by delivering the compound, a method of immunotherapy comprising the compound, a method of immunotherapy comprising the atribed, an immune effector cell that has come raised in vitro or in vivo in the presence and at the expense of an atrigen presenting cell that presents the immunogenic compound in the context of an MHC (major histocompatibility complex) molecule and a method of adoptive immunotherapy comprising administering the immune response to the synthetic and naturally occurring compounds. The compounds are useful for modulating an immune response to the synthetic and naturally occurring components of anti-cancer vaccines. The compounds are useful for treating cancer, particularly covarian cancer. The compounds are also useful for generating antibodies that specifically recognise and bind to these molecules. These compounds are also useful for antibodies are useful in diagnostic methods for the detection and purification of antibodies, or as immunogens for the production of antibodies. The present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Note: Immunogenic ligands AAU74681-AAU74686 are stated to be encoded by the degenerate DNA sequences AAS20120-AAS20125 respectively but have not been cross-referenced or CDS features put in due to the degeneracy of the DNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemia.
                                                                   New therapeutic compounds comprising immunogenic ligands, useful for modulating an immune response, particularly for treating ovarian cancer, and as components of anticancer vaccines
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87.5%; Score 56; DB 23; Length 9; 88.9%; Pred. No. 9.3e+05;
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                                                                                                                                                            English.
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26-JAN-2001; 2001US-0770160.
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                                                                                                                                                            Claim 3; Page 55; 68pp;
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                                   WPI; 2002-097764/13.
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Matches 8; Conser
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Nicolette CA;
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LIVELLINE, TEAGLES to INVEST INUMENT STATEMENT PROPERTIES.

DOTYPEPTIGES and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the mucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. They and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopolesis, and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or nerve tissue growth or regeneration; immune suppression and/or stimulation, as anti-inflammatory agents; and in treatment of leukaemias. AAU2510-AAU3304 represent the amino acid in reatment of leukaemias. AAU2510-AAU3304 represent the amino acid sequences of novel human secreted proteins of the invention.
                                                                                                                     Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy -
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                                                                                                                                                                                                                invention relates to novel human secreted polypeptides. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70.3%; Score 45; DB 22; Length 556; 75.0%; Pred. No. 96; ive 0; Mismatches 2; Indels
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                                                                                                                                                                              Claim 20; Page 534; 765pp; English.
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                                                    Liu C, Drmanac RT
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11-JUL-2000; 2000US-0614150.
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                                                                                     WPI; 2001-611725/70.
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Best Local Similarity
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                 (HYSE-) HYSEQ INC.
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                                                   Tang YT,
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capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to polynucleotides encoding novel human proteins or their active domains. The polypeptides, polynucleotides and antibodies raised against the polypeptides are used in a method of treatment of a mammal and prevention of disorders caused by the aberrant protein expression or activity. The polypeptides can be used as
                                                                                                                                                                                                                                The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
genes from Drosophila and for elucidating cell signalling and cell-cell
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                                                                                       The invention relates to an isolated nucleic acid detection reagent
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                                                     Disclosure; SEQ ID NO 183; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                       Length 512,
                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                         68.8%; Score 44; DB 22;
83.3%; Pred. No. 1.2e+02;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                        512 AA;
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molecular weight markers, food supplements, and in antibody production. The polypeptides are used to identify compounds which bind to the polypeptides. Polymucleotides of the invention are used as probes and primers, for sequencing, for chromosome or gene mapping, in the production of recombinant proteins, and in generating anti-sense DNA or production of recombinant proteins, and in generating anti-sense DNA or RNA and in gene therapy. Polypeptides of the invention can be used to target drugs to a tumour, in assays to determine biological activity, to raise antibodies/elicit an immune response, to determine quantitative protein levels, as tissue markers, and to isolate receptors or ligands. Co protein levels, as tissue markers, and to isolate receptors or ligands. Co protein levels, stem cell disorders, regenerating bone, cartilage, tendon, cligament and/or nerve tissue, wound healing, treating burns, promoting contraceptive, treating osteoporosis and osteoarthritis, anaemia, contraceptive, treating osteoporosis and osteoarthritis, anaemia, alerganis, stroke, immune deficiencies resulting from bacterial, viral or fungal infection or from autoimmunity cancer, allergy, asthma, or man, and infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid detection reagent expable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                     Length 554;
                                                                                                                                                                                                                                                  The present sequence represents a protein of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster polypeptide SEQ ID NO 5304.
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Pred. No. 1.3e+02;
0; Mismatches 1;
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83.3%;
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11-JUL-2000; 2000US-0614150.
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Best Local Similarity
5; Conserve
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N-PSDB; ABL03607.
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                                                                                                                                                                                                                                                                             554 AA;
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                                                                                                                      The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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insecticides, therapeutics and pharmaceutical drugs. The invention
discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
                          discloses genomic DNA sequences (ABL16176-ABL10511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 68.8%; Score 44; DB 22; Length 684; Best Local Similarity 62.5%; Pred. No. 1.6e+02; Matches 5; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                              Length 683;
                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster polypeptide SEQ ID NO 786.
                                                                                                                                                                                                                                                                                                              68.8%; Score 44; DB 22;
62.5%; Pred. No. 1.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB57998 standard; Protein; 684 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                            2 LHKWHWYV 9
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                                                                                                                                                                                                                                                      683 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ABL02101
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                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                  Query Match
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This protein is a prophenol oxidase derived from a domestic silkworm. The phenol oxidase may be used as a novel labelling oxidase. The elucidation of the primary structure of the prophenol oxidase will contribute to the reconstitution of a prophenol oxidase activation system which can be applied to the detection of microorganisms by measurement of beta-1,3-glucan and peptide glycan.
         oxidase; prophenol; phenol; domestic silkworm; label; detection
                                                                                                                                                                                                                                                                                       (Pro)phenol oxidase derived from a domestic silkworm - useful labelling oxidase and in pro-phenol oxidase activation system detection of microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 62.5%; Score 44; DB 18; Length 685; Similarity 62.5%; Pred. No. 1.6e+02; 5; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus aureus cellular proliferation protein #333.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antisense, prokaryotic cellular proliferation protein, antibiotic, antibacterial, drug design.
                                                                 1..52
/label= pro-sequence
53..685
/label= phenol_oxidase
/note= "claim_""
                                                                                                                                                                                                                                                                                                                                      Claim 2; Page 14-17; 18pp; Japanese.
                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU34057 standard; Protein; 142 AA.
                                                                                                                                                                                                                                (WAKP ) WAKO PURE CHEM IND LTD.
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23-MAY-2000; 2000US-206848P.
26-MAY-2000; 2000US-207727P.
                                                                                                                                                                                    95JP-0177444.
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                                                                                                                                                                                                                                                     WPI; 1997-148588/14.
N-PSDB; AAT62660.
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                           685 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200170955-A2.
                                                                                                                                      JP09023886-A.
                                                                                                                                                                                    13-JUL-1995;
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                                 Bombyx mori.
                                                                                                                                                             28-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                        Key
Peptide
                                                                                          Protein
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AAU34057
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Pro) phenol:oxidase from silkworm - useful as a labelling oxidase
                                                                                                                                                                                  Silkworm; larvae; pro; phenoloxidase; Phe52-Val693; Phe52-Gly685 labelling oxidase.
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                                                                                                                                                             Bombyx mori (pro)phenoloxidase Phe52-Gly685.
                                                                                                                                                                                                                                                                                                   41..51
/note= "peptide fragment"
                                                                                                                                                                                                                                                                                       "peptide fragment"
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                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                          AAR89115 standard; Protein; 685 AA.
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                                                                                                                                                                                                                                                                                                                         52..61
/note= '
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                                206 ІННИНИН 213
            LHKWHWYV 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   685 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prophenol oxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAR89115
                                                                                                                                                                                                                                                                                                                                                           JP07289251-A.
                                                                                                                                                                                                                                                                                                                                                                                                          22-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                22-APR-1994;
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                                                                                                                                                                                                                      Bombyx mori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                AAR89115;
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                                                                                                                                                                                                                                                       Peptide
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ID AAW:

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AC AAW:

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Haselbeck R,
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08-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABP39358;
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ABP39358
%X86666666666666666688XXXXXXXX
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                                                                                                                                                                                                                                                                                                                                                                                The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are genes themselves and the encoded proteins. The proteins used in the proteins are set also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen of for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an avide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Cof the printed specification, but was obtained in electronic form part directly from MIPO at
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                                                                                                                                              Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                               New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67.2%; Score 43; DB 22; Length 142; 75.0%; Pred. No. 50; 1; Indels 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus aureus cellular proliferation protein #946.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                                                     Example 3; Seq ID No 5553; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU36776 standard; Protein; 147 AA.
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23-MAY-2000; 2000US-206848P.
26-MAY-2000; 2000US-207727P.
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                  27-NOV-2000; 2000US-253625F.
22-DEC-2000; 2000US-257931F.
16-FEB-2001; 2001US-269308F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                            (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus aureus
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21 LHNFHWYV 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 LHKWHWYV 9
                                                                                                                                                                                                                      2001-611495/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             142 AA;
                                                                                                                                                                                                                                             N-PSDB; AAS51916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200170955-A2.
                                                                                                                                                     Haselbeck R,
Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-FEB-2002
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Matches
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AAU36776
XX
AC AAU36
XX
DT 14-FE
XX
XX
DE Staph
XX
KW Antis
KW Antis
KW Antis
XX
COS
Staph
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COS
S
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in their use in identifying the comparation of genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are genewindrae, Pseudomonas aeruginosa and Enterococcus facefals. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to invention at some used in proliferation of potential new targets and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The proteins can be used to screen sequence represents an essential prokaryotic cellular proliferation protein.

When the printed specification, but was obtained in electronic compared to the printed specification, but was obtained in electronic
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                                                                                                                                                                                                                                                            Carr GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:4203.
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                                                                                                                                                                                                                                                            Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h similarity 75.0%; Score 43; DB 22; Length 147; Similarity 75.0%; Pred. No. 52; Length 147; 6; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                            Zyskind JW, Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; Seq ID No 12369; 511pp; English
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23-OCT-2000; 2000US-242578P.
27-WOV-2000; 2000US-253625P.
22-DBC-2000; 2000US-253731P.
16-PBB-2001; 2001US-269308P.
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97US-064964P
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                                                                                                                                                                                                                                                            Ohlsen KL,
Xu HH;
                                                                                                                                                                                     (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          || :||||
25 LHNFHWYV 32
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Best Local Similarity
Matches 6; Conserv
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The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus pyogenee), comprising one of 5481 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Wucleic acids encoding (I) are used to detect Streptococcus in a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromosome processes and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                         67.2%; Score 43; DB 23; Length 235;
40.0%; Pred. No. 82;
iive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 20; SEQ ID No 50065; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human diagnostic protein #19697.
                Claim 1; Page 3373; 4525pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABG19706 standard; Protein; 1248 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 FLHKW-----HWYV 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
                                                                                                                                                                                                                                                                                                                                                                     Streptococcus proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-639362/73.
N-PSDB; AAS83893.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                         235 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus, GAS, GBS, group B streptococcus, Streptococcus agalactiae, group A streptococcus, Streptococcus pyogenes, antibacterial, antiinflammatory, infection, vaccine, meningitis, gene therapy.
                                                                                                                                                                                                                       ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection.

N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                 Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
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                                                                                                                                                                                       Disclosure; SEQ ID 4203; 267pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABP26523 standard; Protein; 235 AA.
  (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-OCT-2001; 2001WO-GB04789.
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24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GB-0005640.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CHIR-) CHIRON SPA. (GENO-) INST GENOMIC RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Masignani V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Conservative
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43 LHNFHWYV 50
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                                                                          WPI; 2002-381255/41.
N-PSDB; ABN91903.
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Best Local Similarity
                                      Doucette-Stamm LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  166 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                             USPTO web site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200234771-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABP26523;
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8 염

Gaps

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Yeast, protein-protein interaction, Selected Interacting Domain, SID (RTM); secretion yield; cancer; neurodegenerative disease; fungicide; cytostatic; neuroprotective.
                                                                                                                                                                                                                       Yeast selected interacting domain protein SEQ ID NO: 110.
                                                                                                                                                                                     ABJ10988 standard; Protein; 98 AA.
                                                                                                                                                                                                                                                                                            14-FEB-2002; 2002WO-EP02299.
                                                                                                                                                                                                                                                                                                        16-FEB-2001; 2001US-269266P
                                                                                                                                                                                                                                                           Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                   (HYBR-) HYBRIGENICS
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                                                                                                                                                                                                             10-DEC-2002
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Matches
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(first entry)

The present invention relates to complexes between Saccharomyces cerevisiae Selected Interacting Domain (SID (RTM)) proteins and coding sequences. The protein complexes of S. cerevisiae are useful in drug development, in screening drugs or agents that modulate the interaction of proteins, for developing yeast strains with better secretion yield of

drug screening or development, for developing yeast strains with better secretion yield of protein, or in gene therapy (e.g. to treat Candida infection or cancer) New protein-protein complexes of Saccharomyces cerevisiae, useful in

WPI; 2002-674913/72. N-PSDB; ABT11305.

Legrain P;

Claim 6; Page 71; 357pp; English.

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condition mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags consideritying expressed genes. (I) is useful in gene therapy techniques constant activity of (II) or to treat disease states involving constantating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical also disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in casponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human DNA and consideration but was obtained in electronic format directly from WIPO expectification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            at ftp.wipo.int/pub/published_pct_sequences
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                                                                     Similarity 100.0%; Pred. No. 49; DB 23; Length 98; Similarity 100.0%; Pred. No. 49; 5; Conservative 0; Mismatches 0; Indels
                                                                                Best Local Similarity
Matches 5; Conserv
                                                                                                                                    74 KWHWY 78
                                                    98 AA;
                                                                                                                 4 KWHWY 8
                                                     Sequence
                                                                        Query Match
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Search completed: December 16, 2003, 14:14:29

: 34 secs

Job time

protein, and in gene therapy. The protein complexes, polypeptides and polynucleotides are useful for preventing or treating Candida infection, cancer or neurodegenerative diseases in humans or animals. The present

sequence is a protein of the invention.

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Sequence 5382, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                            Appli
                                                                                                                                       Sequence Sequence
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                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSES: GENOME THERAPEUTICS CORPORATION STREET: 100 Beaver Street CITY: Waltham
                                                       US-09-537-168-4
US-09-537-168-6
US-09-67-459-2
US-09-636-252A-13
US-09-381-687-6
US-09-381-687-8
                                                                                                                                                                 PCT-US94-01553A-32
PCT-US94-01553A-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/01571
FILING DATE: July 2, 1997
                                                                                                                                                                                               PCT-US95-10426-32
PCT-US95-10426-36
                                                                                                                                                                                                                             US-08-468-220-37
US-08-468-698-37
US-08-194-664A-37
                                                                                                                                                    US-09-545-586-4
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; LOCATION: (B) LOCATION 1...191
; SEQUENCE DESCRIPTION: SEQ ID NO: 5382:
US-09-107-532A-5382
                                                                                                                                                                                                                                                                                                          ALIGNMENTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: PC
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPERENCE/DOCKET NUMBER: G
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 5382:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 191 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLRCULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 7310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Massachusetts
CQUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 02354
OMPUTER READABLE FORM:
RESULT 1
US-09-107-532A-5382
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 Sequence 5382, Ap
Sequence 4203, Ap
Sequence 4, Appli
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                                                                                                    2003, 14:11:00 ; Search time 12.3333 Seconds (without alignments) 30.875 Million cell updates/sec
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Sequence 13
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Sequence 3
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\(\csigma \) \(\csigma 
               GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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-09-134-001C-4203
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S-08-468-220-35
S-08-468-20-36
S-08-468-698-35
S-08-468-698-35
S-08-468-698-35
S-08-600-908A-13
S-08-600-908A-13
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-08-914-679A-3
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US-09-1134-001C-42
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US-09-1134-01
US-09-1133-068-5
US-09-290-133-412-5
US-09-290-133-412-5
US-09-672-459-4
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US-09-672-459-4
US-09-68-55-586-5
US-09-68-50-12
US-08-68-70-12
US-08-468-20-13
US-08-468-20-13
US-08-108-133-13
US-08-108-133-13
US-08-683-833-13
US-08-683-833-13
US-08-683-833-13
US-08-1182-859-2
US-09-1182-859-2
US-09-192-859-2
US-09-193-068-4
US-09-193-068-4
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Match Length
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Pred. No. 67;
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100.0%; Pred. No. c.
                                                                                                    RESULT 4
US-09-170-670-5
Sequence 5, Application US/09170670
Sequence 5, Application US/09170670
RENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben
TITLE OF INVENTION: Alpha-Amylase Mutants
TITLE REFREENCE: 5276.200-US
CURRENT APPLICATION NUMBER: US/09/170,670
CURRENT FILING DATE: 1998-10-13
EARLIER APPLICATION NUMBER: 1172/97
EARLIER PELING DATE: 1997-10-13
SARILER PILING DATE: 1997-10-28
NUMBER OF SEQ ID NOS: 22
SOFTWARR: FastSEQ for Windows Version 3.0
SEGUID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Svendsen, Allan
APPLICANT: Svendsen, Allan
APPLICANT: Kjrulff, S ren
APPLICANT: Bisgaard-Frantzen, Henrik
APPLICANT: Andersen, Carsten
ITILE OF INVENTION: -Amylase Variants
FILE REFERENCE: 5709-000-02
CURRENT APPLICATION NUMBER: US/09/193,068
CURRENT FILING DATE: 1998-11-16
NUMBER OF SEQ ID NOS: 31
SOFTMARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: B. amyloliquefaciens
US-09-170-670-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: B. amyloliquefaciens
US-09-193-068-5
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Best Local Similarity 100.
Matches 5; Conservative
                                         152 KWHWY 156
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4 KWHWY 8
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Patent No. 6380370

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: LYMD DOUGETE-Stamm et al

TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-08-14

NUMBER: OF SEQ ID NOS: 5674

SEQ ID NO 4203

LENGTH: 166
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                Query Match 70.3%; Score 45; DB 4; Length 191; Best Local Similarity 75.0%; Pred. No. 12; Matches 6; Conservative 2; Mismatches 0; Indels
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Pred. No. 20;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Svendsen, Allan
APPLICANT: Svendsen, Allan
APPLICANT: Svendsen, Torben
APPLICANT: Borchert, Torben
APPLICANT: Borchert, Torben
APPLICANT: Borchert, Torben
APPLICANT: Bleggard-Frantzen, Henrik
TILE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 4796.204-US
CURRENT APPLICATION WUMBER: US/09/182,859
CURRENT FILING DATE: 1996-10-29
EARLIER APPLICATION NUMBER: 0712/96
EARLIER APPLICATION NUMBER: 0712/96
EARLIER PILING DATE: 1996-06-28
EARLIER PILING DATE: 1996-06-28
EARLIER PELING DATE: 1996-0719
EARLIER FILING DATE: 1996-0711
EARLIER FILING DATE: 1996-11-08
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Staphylococcus epidermidis US-09-134-001C-4203
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US-09-182-859-4
Sequence 4, Application US/09182859
Patent No. 6143708
GENERAL INFORMATION:
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Best Local Similarity 75.0
Matches 6; Conservative
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52 LHQYHWYV 59
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APPLICANT: Nielsen, Bjarne Ronfeldt
APPLICANT: Nielsen, Vibeke Skovgaard
APPLICANT: Nielsen, Vibeke Skovgaard
APPLICANT: Nielsen, Vibeke Skovgaard
APPLICANT: Hoeck, Lisbeth Hedegaard
TITILE OF INVENTION: No. 6528298el -Amylase And -Amylase Mutants
TILE REPREBREE: 5276,400-US
CURRENT APPLICATION NUMBER: US/09/545,586
CURRENT PILING DATE: 2000-04-07
PRIOR FILING DATE: 1999-04-13
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 65.6%; Score 42; DB 4; Length 480; Best Local Similarity 100.0%; Pred. No. 67; Matches 5; Conservative 0; Mismatches 0; Indels
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APPLICANT: Borchert, Torben
APPLICANT: Bisgard-Frantzen, Henrik
TITLE OF INVENTION: Alpha-Amylase Mutants;
FILE REFERENCE: 4796,204-US
CURRENT APPLICATION NUMBER: US/09/672,459
CURRENT FILING DATE: 1996-10-29
PRIOR APPLICATION NUMBER: 05/182,859
PRIOR PLING DATE: 1996-04-20
PRIOR PILING DATE: 1996-04-30
PRIOR PILING DATE: 1996-07-11
PRIOR PILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FRASEREQ for Windows Version 3.0
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Bisgard-Frantzen Henrik
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/09545586; Patent No. 652829 9; GENERAL INFORMATION: APPLICANT: Svendsen, Allan
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LENGTH: 480
TYPE: PRT 6
ORGANISM: B. amyloliquefaciens
US-09-545-586-5
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Best Local Similarity 100.
Matches 5; Conservative
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US-09-545-586-5
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| Sequence 5, Application US/09290734 |
| Patent No. 6361899 |
| Patent No. 6361899 |
| GENERAL INFORMATION: |
| APPLICANT: Svendsen, Allan |
| APPLICANT: Borchert, Torben Vedel |
| APPLICANT: Untrup, Helle |
| APPLICANT: Outtrup, Helle |
| APPLICANT: Nielsen, Vibeke Skovgaard |
| APPLICANT: Nielsen, Vibeke Skovgaard |
| APPLICANT: Nielsen, Songaard |
| APPLICANT: Heeck, Lisbeth Hedegaard |
| APPLICANT: Hoeck, Lisbeth Hedegaard |
| TILLE OF INVENTION: No. 6361989el -Amylase Mutants |
| FILE REFERENCE: 5276.400-US |
| CURRENT APPLICATION NUMBER: US/09/290,734 |
| CURRENT FILING DATE: 1999-04-13 |
| SOFTWARE: FastSEQ for Windows Version 3.0 |
| LENGTH: 480 |
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                      APPLICANT: Andersen, Carsten
APPLICANT: Nielsen, Bjarne
APPLICANT: Nielsen, Djarne
APPLICANT: Niesen, Torben L.
TITLE OF INVENTION: Alpha-Amulase Mutants
FILE REFERENCE: 5369.200-028
FURRENT APPLICATION NUMBER: US/09/183,412
CURRENT FILING DATE: 1998-10-30
BARLIER APPLICATION NUMBER: 60/093,234
BARLIER FILING DATE: 1997-11-06
BARLIER FILING DATE: 1997-10-30
BARLIER FILING DATE: 1997-10-30
BARLIER FILING DATE: 1998-0-17
BARLIER APPLICATION NUMBER: 1240/97
BARLIER FILING DATE: 1998-0-14
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FASTSEQ for Windows Version 3.0
SSERIOTH 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Bacillus amyloliqufaciens
US-09-183-412-5
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Patent No. 6436888
GENERAL INFORMATION:
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; ORGANISM: B. amyloliquefaciens
US-09-290-734-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 65.6
Best Local Similarity 100.
Matches 5; Conservative
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US-09-672-459-4
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                                                            Length 483;
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                                                                                                                                                                                                                                                                                                                       RESULT 12
US-08-468-220-32
is Sequence 3.2, Application US/08468220
is Sequence 3.2, Application US/08468220
is Patent No. 5824532
is GENERAL INFORMATION:
is APPLICANT: Antrim, Richard L.
is APPLICANT: Mitchinson, Colin
is APPLICANT: Power, Scott D.
is APPLICANT: Solheim, Leif P.
if TILE OF INVENTION: Oxidatively Stable Alpha-Amylase
in NUMBER OF SEQUENCES: 68
is CORRESPONDENCE ADDRESS:
is ADDRESSER Genemoor International, Inc.
is STREET: 180 Kimball Way
is CITY: South San Francisco
                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
COMPUTER: 1EM PC compatible
COMPUTER: 1EM PC compatible
COMPUTER: 1EM PC compatible
COMPUTER: 0.000 Ms. 10.000
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 0.000 Ms. 20
FILING DATE: 0.000 Ms. 20
FILING DATE: 10.000 Ms. 20
FILING DATE: 20
FILING DATE: 20
FILING DATE: 20
FILING DATE: 10.000 Ms. 20
FILING DATE: 2
                                                            Score 42; DB 1;
Pred. No. 68;
                                      65.6%; Scor.
100.0%; Pred. No. co.
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                                                         Query Match
Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-468-220-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                           154 KWHWY 158
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US-08-468-220-36
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US-08-645-971-2
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Patent No. 5763385

GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Modified Alpha-Amylases Having Altered
TITLE OF INVENTION: Calcium Binding Properties
TITLE OF INVENTION: Calcium Binding Properties
COMPUTER READABLE FORM:
MUMBER OF SEQUENCES:
COMPUTER READABLE FORM:
MUMBER OF SEQUENCES:
COMPUTER PREPAIR FORM:
MEDIUM TYPE: Floppy disk
COMPUTER PREPAIR FORM:
COMPUTER PREPAIR FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER PREPAIR FORM:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/645,971
INFORMATION FOR SEQ ID NO: 2:
BEQUENCE CHARACTERISTICS:
INFORMATION POR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
INFORMATION CALCIUM AND ACIDE
TYPE: Amino acide
                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.C..
COUNTRY: U.C..
COUNTRY: U.C..
ZIP: 94080
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Batentin Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,700
FILING DATE: 06-JUN-1995
CLASSIFICATION: 252
ATTORNEY/AGENT INNORMATION:
NAME: Stone, Christopher:
REGISTRATION NUMBER: GC275
TELEPHONE: (415) 742-727
TELEPHONE: (415) 742-727
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: AMINO acid
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65.6%; Score 42; DB 1; Length 483; 100.0%; Pred. No. 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
         APPLICANT: COLIN MITCHINSON
APPLICANT: CAROL A. REQUADT
APPLICANT: TRACI H. ROPP
APPLICANT: LEIF P. SOLHEIM
ITLE OF INVENTION: MUTANT ALPHA-AMYLASE
NUMBER OF SEQUENCES: 4 0
CORRESSONDENCES: 4
ADDRESSEE: Genencor International
STREET: 180 Kimball Way
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Prea. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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SENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                             STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
US-08-645-971-2
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DB 2; Length 483; 68;
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APPLICANT: Barnett, Christopher
APPLICANT: Barnett, Christopher
APPLICANT: Mitchinson, Colin
APPLICANT: Mitchinson, Colin
APPLICANT: Requadt, Carol
APPLICANT: Requadt, Carol
APPLICANT: Solheim, Leif P.
TITLE OF INVENTION: Oxidatively Stable Alpha-Amylase
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International, Inc.
STREET: 180 Kimball Way
CITY: South San Francisco
STATE: CA
                                                                                                                                                                                                                                                                                                                    O'DERATING SYSTEM: FC-LUCS/ms-LUCS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,698
FILING DATE: 06-JUN-95
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/194,664
FILING DATE: 10-FEB-94
PRIOR APPLICATION NUMBER: 08/016,395
FILING DATE: 11-FEB-93
ATTORNEY/AGENT INFORMATION:
NAME: Stone, Christopher L.
REGISCHATION NUMBER: 35,696
REFRENCEY/DOCKET NUMBER: 35,696
REFRENCEY/DOCKET NUMBER: 35,696
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ ID NO: 32:
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
GURRENY APPLICATION NATA:
APPLICATION NUMBER: US/08/468,698
FILING DATE: 06-JUN-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 65.6%; Score 42; DB Best Local Similarity 100.0%; Pred. No. 68; Matches 5; Conservative 0; Mismatches
                                                                                                                                                  ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 35 inch, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5849549
       STREET: 180 Kimball Way
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 483 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-698-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154 KWHWY 158
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USA
                                                                                                                       USA
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                                                                                                                       COUNTRY:
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                                                                                                                       APPLICANT Barnett, Christopher
APPLICANT Barnett, Christopher
APPLICANT Bruchison, Colin
APPLICANT Requadt, Carol
APPLICANT Requadt, Carol
APPLICANT SEQUENCES:
APPLICANT SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: 180 Kimball Way
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 32, Application US/08468698
; Patent No. 5845549
; GENERAL INFORMATION:
APPLICANT: Antrim, Richard L.
APPLICANT: Mitchinson, Colin
APPLICANT: Power, Scott D.
APPLICANT: Solheim, Leif P.
TITLE OF INVENTION: Oxidatively Stable Alpha-Amylase
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSER: Genencor International, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/468,220
FILING DATE: 06-JUN-95
CLASSIFTCATION: 435
FILING DATE: 106-JUN-95
CLASSIFTCATION DATA:

APPLICATION NUMBER: 08/194,664

FILING DATE: 11-FEB-94

ATORNEY/AGBNT INFORMATION:

NAME: SLOOME, Christopher L.

REGISTRATION NUMBER: 35,696

REFERENCE/DOCKET NUMBER: GC220D1
TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 742-7555

TELEPHONE: (415) 742-7555

TELEPHONE: (415) 742-7555

TELEPHONE: (415) 742-7555

TELEPHONE: (415) 742-7515

SEQUIDENCE CHARACTERISTICS:

SEQUIDENCE CHARACTERISTICS:

TEMPORMATION FOR SEQ ID NO: 36:

SEQUIDENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIF: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING TO TANKE TO THE THE TO THE T
Sequence 36, Application US/08468220
                                                                                                       APPLICANT: Antrim, Richard L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 483 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
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STRANDEDNESS: si
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CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/194,664

FILING DATE: 10-FEB-94

PRIOR APPLICATION NUMBER: 08/016,395

FILING DATE: 11-FEB-93

ATTORNEY/AGENT INFORMATION:

NAME: Stone, Christopher L.

REGISTRATION NUMBER: GC220D2

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPAX: (415) 742-755

INFORMATION POR SEQ ID NO: 36:

SEQUENCE CHARACTERISTICS:

INFORMATION POR SEQ ID NO: 36:

TELEFAX: (415) 742-755

INFORMATION POR SEQ ID NO: 36:

TELECOMMUNICATION INFORMATION POR SEQ ID NO: 36:

TOPOLOGY: linear

MOLECULE TYPE: annio acids

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-468-698-36

QUENTY MATCH

QUENTY MATCH

GOGS: (%; SCOIT 42; DB 2; Length 483;

Best Local Similarity 100.0%; Pred. NO: 68;

MATCHES 5; CONSERVATIVE 0; Indels 0; Gaps 0;
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Search completed: December 16, 2003, 14:20:40 Job time : 12.3333 secs

4 KWHWY 8 ||||| 154 KWHWY 158

g 8

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APPLICANT: Charles A. Nicolette
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS FOR OVARIAN CANCER
FILE REFERENCE: 68126881209900
CURRENT APPLICATION NUMBER: US/09/870,089B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 FLHKWHWYV 9
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Best Local Similarity
Matches 9; Conserv
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Sequence 4, Appli
Sequence 8, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 30, Appli
Sequence 30, Appli
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Sequence 7, Appli
Sequence 5553, Ap
Sequence 12369, A
Sequence 5, Appli
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                                                                                                 December 16, 2003, 14:18:11; Search time 22.1667 Seconds (without alignments) 75.512 Million cell updates/sec
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| cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO6_NEW PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO7_NEW PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USO7_NEW PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USO7_NEW PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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2 US-09-870-089B-7

US-09-815-242-5553

US-09-615-242-12369

US-09-769-864-5

US-09-769-864-4

US-09-769-864-4

US-09-854-346-8

US-09-854-346-8

US-09-918-543-10

US-09-918-543-10
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                                                                                                                                                                                                                                                                                                               684280 segs, 185983659 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                     - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Match Length
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Perfect score:
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Maximum DB seq
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Sequence 4, Appli
Sequence 6, Appli
Sequence 7, Appli
Sequence 2, Appli
Sequence 114, Appl
Sequence 21, Appli
Sequence 21, Appli
Sequence 21, Appli
Sequence 22, Appli
Sequence 302, Appl
Sequence 302, Appli
Sequence 302, Appli
Sequence 5214, Appli
Sequence 693, Appli
Sequence 693, Appli
Sequence 693, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
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Sequence 33052, Appli
Sequence 3, Appli
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Publication No. US200301752541
GENERAL INFORMATION:
APPLICANT: Charles A Micolette
TITLE OF INVENTION THERAPEUTIC COMPOUNDS FOR OVARIAN CANCER
FILE REPRENEUE: 60126081209900
CURRENT APPLICATION NUMBER: US/09/870,089B
CURRENT FILEMC DAIE: 2001-05-30
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2 US-10-186-042-2

5 US-10-146-32-4

2 US-10-146-32-6

2 US-10-105-733-8

2 US-10-108-733-8

2 US-10-184-771-2

2 US-10-189-922-2

5 US-10-189-922-114

2 US-10-184-771-4

2 US-10-184-771-4

2 US-09-972-618-24

US-09-732-618-24

US-09-732-618-24

US-09-732-618-24

US-09-732-618-24

US-09-732-618-24

US-09-732-618-24

US-09-132-618-25

US-09-132-618-25

US-09-132-618-25

US-09-132-618-25

5 US-10-125-567A-302

5 US-10-126-761-9146

5 US-10-156-761-9146

5 US-10-156-761-9146

5 US-10-156-761-9146

5 US-10-156-761-9146

5 US-10-156-761-9146

5 US-10-186-913-9146

5 US-10-186-913-9146

5 US-10-186-913-9146

5 US-10-186-913-914
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US-09-815-242-13494
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 9
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 7, Application US/09870089B; Publication No. US20030175252A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; CTHER INFORMATION: ATF4/CREB-2
US-09-870-089B-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
  Conservative
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GENERAL INFORMATION:
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Best Local Similarity 75.0%; Pred. No. 73;
Matches 6; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Obligation, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Zyskind, Judith W.
APPLICANT: Tranic, John D.
APPLICANT: Tranic, John D.
APPLICANT: Tranic, John D.
APPLICANT: Yamamoro, Mobert T.
APPLICANT: Yamamoro, Mobert T.
APPLICANT: Xu. H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-22
PRIOR PELLORITON NUMBER: 60/259,308
PRIOR FILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: 60/259,308
PRIOR PELLORITON NUMBER: 60/250,308
PRIOR PELLORITON NUMBER: 60/250,308
PRIOR PELLORITON NUMBER: 60/250,301
PRIOR PELLORITON NUMBER: 60/250,301
PRIOR PELLORITON NUMBER: 60/250,301
                                                                                                                                                                                                                                                                                                                                                                          Query Match 87.5%; Score 56; DB 12; Length 9; Best Local Similarity 88.9%; Pred. No. 6.1e+05; Matches 8; Conservative 0; Mismatches 1; Indels
CURRENT FILING DATE: 2001-05-30
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 7
LENGTH: 9
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; Sequence 12369, Application US/09815242
; Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5553, Application US/09815242 Patent No. US20020061569A1 GENERAL INFORMATION: APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Staphylococcus aureus US-09-815-242-5553
                                                                                                                                                                                                                                                   ; FEATURE:
; OTHER INFORMATION: ATF4/CREB-2
US-09-870-089B-7
                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
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21 LHNFHWYV 28
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US-09-815-242-5553
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LENGTH: 142
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                APPLICANT: Haselbeck, Korert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Ohlsen, Kari L.
APPLICANT: Oskind, Judith W.
APPLICANT: Zyskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Tramacto, Robert T.
APPLICANT: APRINCE Carr, Grant J.
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
TITLE OF INVENTION: Prokaryotes
TITLE OF INVENTION: Prokaryotes
FILB REFERENCE: EllTRA. 011A
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PLING DATE: 2000-03-24
PRIOR PLING DATE: 2000-05-23
PRIOR PLING DATE: 2000-05-24
PRIOR PLING DATE: 2000-05-24
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-11-27
PRIOR PPLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-10-24
PRIOR PLING DATE: 2000-10-24
PRIOR PLING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE FEASTSCO for Windows Version 4.0
SOFTWARE FEASTSCO for Windows Version 4.0
SEQ ID NO 12369
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APPLICANT: Borchert, Torben V.
APPLICANT: Svendsen, Carsten
APPLICANT: Andersen, Carsten
APPLICANT: Nissen, Torben L.
APPLICANT: N
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SOFTWARE: FaetSEQ for Windows Version 3.0
SEQ ID NO 80
LENGTH: 480
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APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25 LHINFHWYV 32
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US-09-769-864-5
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Sequence 8. Application US/09854346

Sequence No. US20020068352A1

GENERAL INFORMATION:

APPLICANT: No. US20020068352A10zymes A/S

APPLICANT: Svendsen, Allan

APPLICANT: No. US20020068352A10zymes A/S

APPLICANT: Nelsen, Bjarne Ronfeldt

TITLE OF INVENTION: Alpha-amylase variants with altered 1,6 activity

FILE REFERENCE: 6140.200-US

CURRENT APPLICATION NUMBER: US/09/854,346

CURRENT APPLICATION NUMBER: US/09/854,346

MUMBER OF SEQ ID NOS: 15

SOFTWARE: Patentin version 3.1

FERSO ID NO 8.

FERSO ID NO 8.

FERSO ID NO 8.
                            Gaps
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APPLICANT: Svendsen, Allan
APPLICANT: Orgensen, Christel Thea
APPLICANT: Nielsen, Glarne Ronfeldt
TITLE OF INVENTION: Alpha-amylase variants with altered 1,6 activity
FILE REFERENCE: 6140.200-US
CURRENT APPLICATION NUMBER: US/09/854,346
CURRENT PILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.1
SEQ ID NO 10
LENGTH: 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 65.6%; Score 42; DB 9; Length 483; Best Local Similarity 100.0%; Pred. No. 2.7e+02; Matches 5; Conservative 0; Mismatches 0; Indels
                            0: Indels
100.0%; Pred. No. 2.7e+02; tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 10, Application US/09854346; Patent No. US20020068352A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT; ORGANISM: Bacillus licheniformis
US-09-854-346-8
  Best Local Similarity 100.0
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                            APPLICANT: Standard, Aliah
APPLICANT: Standard
APPLICANT: Borchert, Torben
APPLICANT: Bisgard-Frantzen, Henrik
TITIE OF INVENTION: Alpha-Amylase Mutants
TITIE REFERENCE: 4796,204-US
CURRENT APPLICATION NUMBER: US/10/186,042
CURRENT FILING DATE: 2002-06-28
PRIOR FILING DATE: 1998-10-29
PRIOR FILING DATE: 1998-10-29
PRIOR FILING DATE: 1998-10-29
PRIOR FILING DATE: 1996-04-30
PRIOR FILING DATE: 1996-04-30
PRIOR FILING DATE: 1996-04-30
PRIOR FILING DATE: 1996-07-11
PRIOR FILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FASLSEQ FOR WINDOWS Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Svendsen, Allan
APPLICANT: Andersen, Carsten
APPLICANT: Nielsen, Bjarne
APPLICANT: Nissen, Torben L.
APPLICANT: Nissen, 100,769,864
CURRENT APPLICATION NUMBER: 09/183,412
PRIOR APPLICATION NUMBER: 09/183,412
PRIOR FILING DATE: 1999-10-30
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FRSESEQ FOR WINGOWS VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Bacillus amyloliquefaciens
US-10-186-042-4
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; Patent No. US20010039283A1
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
                                                                                                                                                                                                                         Sequence 4, Application US/10186042; Publication No. US20030171236A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ; ORGANISM: Bacillus licheniformis US-09-769-864-4
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LENGTH: 483
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US-09-769-864-4
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Gaps

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0; Indels

65.6%; Score 42; DB 10; 1 100.0%; Pred. No. 2.7e+02; iive 0; Mismatches 0;

Length 483;

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TYPE: PRT CORGANISM: Bacillus licheniformis US-09-918-543-30
                                                                                                                                                Query Match 65.6 Best Local Similarity 100. Matches 5; Conservative
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US-09-925-576C-8
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LENGTH: 483
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APPLICANT: No. US20020155574Alozymes A/S
APPLICANT: Thisted, Thomas
APPLICANT: Kjaerulff, Soren
APPLICANT: Kjaerulff, Soren
APPLICANT: Andersen, Carsten
APPLICANT: Andersen, Carsten
FILE REFERENCE: 10062-200-US
FILE REFERENCE: 10062-200-US
CURRENT APPLICATION NUMBER: US/09/918,543
CURRENT FILING DATE: 2001-07-31
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.1
SEQ. ID NO 8
LENGTH: 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10, Application US/09918543

Sequence 10, Application US/09918543

Sequence 10, Application US/09918543

Sequence 10, Application US/002015574A1

Septicant: No. US20020155574A1

APPLICANT: Thisted, Thomas

APPLICANT: Andersen, Carsten

APPLICANT: Puglsang, Claus Crone

ITILE REFERENCE: 10662.200-US

CURRENT APPLICATION NUMBER: US/09/918,543

CURRENT FILING DATE: 2001-07-31

NUMBER OF SEQ ID NOS: 30

SOFTWARE: Patentin version 3.1

SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 30, Application US/09918543
Fatent No. US20020155574A1
GENERAL INFORMATION:
APPLICANT: No. US20020155574A102ymes A/S
APPLICANT: Thisted, Thomas
APPLICANT: Thisted, Thomas
APPLICANT: Kjaerulff, Soren
APPLICANT: Andersen, Carten
APPLICANT: Andersen, Carten
APPLICANT: Puglsang, Claus Crone
TITLE OF INVENTION: Alpha-amylase mutants with altered properties
FILE REFERENCE: 10062.200-US;
CURRENT APPLICATION NUMBER: US/09/918,543
CURRENT PILING DATE: 2001-07-31
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.1
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100.0%; Pred. No. 2.7e+02;
vative 0; Mismatches 0;
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; ORGANISM: Bacillus amyloliquefaciens
US-09-918-543-10
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; ORGANISM: Bacillus licheniformis
US-09-918-543-8
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Best Local Similarity 100.د
ادم 5; Conservative
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US-09-918-543-30
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                                                                                                                                      Sequence 8, Application US/09925576C
Publication No. US20030129718A1
GENERAL INFORMATION:
APPLICANT: Borchert, Torben Vedel
APPLICANT: Nielsen, Blarne Ronfeldt
FTLIE REFERENCE: 10004.204-US
CURRENT APPLICATION UNBER: US/09/925,576C
CURRENT FILING DATE: 2001-08-09
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Version 3.1
SEQ ID NO 8
IENGTH: 483
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Sequence 10, Application US/0992576C

Publication No. US20030129718A1

GENERAL INFORMATION:

APPLICANT: Andersen, Carsten

APPLICANT: Nielsen, Bjarne Ronfeldt

TAPLICANT: Nielsen, Bjarne Ronfeldt

TAPLICANT: Nielsen, Bjarne Ronfeldt

TAPLICANT: Nielsen, Byarne Ronfeldt

STREERERENCE: 10004.204-US

CURRENT FILING DATE: 2001-08-09

NUMBER OF SEQ ID NOS: 20

SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Bacillus amyloliquefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-09-925-576C-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 100.
154 KWHWY 158
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RESULT 15

US-10-184-771-13

Sequence 13, Application US/10184771

Publication No. US20030170769A1

GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben Vedel
TILLE OF INVENTION: Alba-Amylase Mutants
FILE REPERENCE: 0776/1F216-US2
CURRENT PILING DATE: 2002-06-28

FRIOR PELLORATION NUMBER: US/10/184,771

CURRENT APPLICATION NUMBER: US/20/636,252

FRIOR PELLOR PELLORATION NUMBER: 08/683,838

FRIOR PELLOR PILING DATE: 2000-08-10

FRIOR FILING DATE: 1996-07-18

NUMBER OF SEQ ID NOS: 16

SEQ ID NO 13

LENGTH: 483

TYPE: PRY

CORGANISM: Bascillius

US-10-184-771-13

Query Match
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Search completed: December 16, 2003, 14:41:06 Job time: 22.1667 secs

4 KWHWY 8 ||||| 152 KWHWY 156

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GenCore version 5.1.6
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OM protein - protein search, using sw model

December 16, 2003, 14:10:15 ; Search time 10.3333 Seconds Run on:

(without alignments) 83.760 Million cell updates/sec

US-09-870-089B-9 1 FLHKWHWYV 9 Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283308 segs, 96168682 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pir 76:*
1: pir1:*
2: pir2:*
3: pir3:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SIMMARIES

					SUMMARIES	
Result No.	Score	% Query Match	Length	DB	ID	Description
1	45	70.3	153	2	G69660	metal-regulated pr
C	44			ď	H69618	stress- and starva
٣	44	68.8		7	C75311	conserved hypothet
4	44	68.8		N	T51430	dolichyl-phosphate
'n	44	68.8		7	871751	dolichyl-phosphate
9	43	67.2		N	H90007	general stress pro
7	43	67.2		~	A87628	conserved hypothet
æ	43	•		~	G82786	conserved hypothet
σ	43	67.2		N	PT0060	N-acetylphosphinot
10	43	67.2		C4	A47031	bialaphos acetylhy
11	43	67.2		Н	BHTLA	hemocyanin chain a
12	42	65.6		N	T16945	hypothetical prote
13	42	65.6		ч	ALBSL	alpha-amylase (EC
14	42	65.6		Н	ALBSN	
15	42	65.6		Н	BHTLE	hemocyanin chain e
16	42	65,6		N	S67964	hemocyanin chain 6
17	41	64.1		N	A11904	hypothetical prote
18	41	64.1		~	AG2462	
19	41	64.1		~	AF2129	ical
20	41	64.1		~	G88979	4
21	40	'n,		7	B83777	stress- and starva
22	40	ď		~	S28082	vif protein - simi
23	40	62.5		~	G75174	hypothetical prote
24	40	62.5		N	H71039	
25	40			Н	BHTLD	Z
26	40	ä		Н	BHHC2A	hemocyanin subunit
27	39	ö		~	T50986	hypothetical prote
28	39	60.9	393	N	C89961	
53	39	6.09		N	H87347	

ALG6 protein - yea	hypothetical prote	TCM10 protein - ye	hypothetical prote	transposase [impor	unknown in ISIN [i	bacterioferrin F1	enterohemolysin 2	hypothetical prote	hypothetical prote	hypothetical prote	spore coat polysac	probable membrane	phosphodiesterase/	probable exported	hypothetical prote
S61985	F95871	S61147	T15576	E90791	A85652	780097	JN0846	T37187	A99775	D85637	E69717	S19439	AC2085	AB0005	T22351
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544	582	611	686	145	145	177	193	200	257	257	339	512	530	569	634
50.9	6.09	6.09	6.09	59.4	59.4	59.4	59.4	59.4	59.4	59.4	59.4	59.4	59.4	59.4	59.4
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AyRelatus: nuclear and sequence not shown; trainstanton not shown.

AyResidues: 1-153 «KUN»

A,Residues: 1-153 «KUN»

A,Residues: 1-153 «KUN»

A,Residues: 1-153 «KUN»

A,Residues: 1-153 «KUN»

A,Resperimental source: strain 168

R;Chen, L.; Helmann, J.D.

Mol. Microbiol. 18, 295-300, 1995

A,Reference number: S70240; MUID:96296451; FMID:8709848

A,Reference number: S70240; MUID:96296451; FMID:8709848

A,Reference number: S70240; MUID:96296451; FMID:8709848

A,Residues: 1-153 «KIR»

A,Residues: 1-153 «KIR»

A,Residues: L.; James, L. L.; James, L. L.; Helmann, J.D.

A,Residues: L.; James, L. L.; Lassell

A,Reference number: A48656; MUID:93374837; PMID:8396117

A,Reference number: A48656; MUID:93374837; PMID:8396110:; PID:g396221

A,Reference number: A48656

A,Reference number: A48656

A,Reference number: A48656

A,Reference number: A44519

A,Reference number: A44519

A,Reference number: A44519

A,Reference number: A44519

A,Residues: 'X',2-15,'KST',19-20,'TVFRMH' «DOW»

. 0

Gaps

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68.8%; Score 44; DB 2; Length 159; 62.5%; Pred. No. 8.1; Live 2; Mismatches 1; Indels
                                                                                                                                                                      ilarity 62.5%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                   11 VHPWHWWV 18
                                                                                                                                                                                                                                                                                              2 LHKWHWYV 9
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                                                                                                                                           Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-498 <SAT>
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C;Genetics:
A;Gene: DR2142
A;Map position: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Bacillus subtlis:
C;Species: Bacon, S; Bruschi, C,V; Caldwell, B; Capuano, V; Carter, N.M; Chorature 350, 249-256, 1997
A;Buthors: Foulger, D; Fritz, C; Fujita, M; Fujita, Y; Fuma, S; Galizzi, A; Galler, Icch, J; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S; Hosono, S; Hullo, M.F. Kochter, P; Koningstein, G; Krogh, S; Rumano, M; Kurita, K.; Lapdus, A.; Laudinois, A; Authors: Lauber, J; Lazarevic, V; Lee, S.M; Levine, A.; Liu, H.; Masuda, S; Maueell, Y; Sado, T.; Scanlon, R; Authors: Schleich, C; Rocha, E; Roche, B; Rose, M; Sadaie, Y; Sato, T; Scanlon, A; Authors: Schleich, S; Schroeter, R; Scoffene, F; Sekiguchi, J; Sekowska, A.; Seror, akeuchi, M; Tamakoshi, A.; Tanaka, T; Targare, P; Yamano, P; Yamano, M; Yamano, K.; Yasunoto, K.; Yata, K.; Yoshida, K.; Witters, P; Wippet, A.; Yamano, K.; Yoshikawa, H.F.; Zumstein, B.; Yoshikawa, H.F.; Zumstein, B.; Zoshikawa, H.F.; Zumstein, B.; Wippet, A.; Wippet, A.; Yamano, C, The Gram-positive bacterium Bacillus subtilis. A; Recession: Hosols
A; Recession: Hosols
A; Recession: Hosols
A; Recession: Hesols
A; Reces
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(Species: Deinococcus radiodurans

(Species: Deinococcus radiodurans

(Species: Deinococcus radiodurans

(Species: O.) Elsen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;

K.; Shalth, H.O.; Venter, J.C.; Fraser, C.M.

S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

A; Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A; Reference number: A75250; MUID:20036896; PMID:10567266
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A;Cross-references: GB:AE002048; GB:AE000513; NID:g6459929; PIDN:AAF11686.1; PID:g645993
A;Experimental source: strain Rl
   A,Note: protein was found to over-accumulate in hydrogen peroxide-resistant mutant strai
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:Z99119; GB:AL009126; NID:g2635411; PIDN:CAB15043.1; PID:g2635549
A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    stress- and starvation-induced gene controlled by sigma-B dps - Bacillus subtilis
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                                                                                                                                                                              70.3%; Score 45; DB 2; Length 153; 75.0%; Pred. No. 5.5; trive 2; Mismatches 0; Indels
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C;Superfamily: hypothetical protein HI1349
                                                                             A;Gene: mrgA
C,Superfamily: hypothetical protein HI1349
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Best Local Similarity 75...
6; Conservative
                                                                                                                                                                                                                    Local Similarity 75.0
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A;Status: preliminary
A;Molecule type: DNA
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C.Accession: 871751
R.Takahashi, M.; Inoue, N.; Ohishi, K.; Maeda, Y.; Nakamura, N.; Endo, Y.; Fujita, T.; 7
R.Takahashi, M.; Inoue, N.; Ohishi, K.; Maeda, Y.; Nakamura, N.; Endo, Y.; Fujita, T.; 7
R.Tatelashi, M.; Inoue, N.; Ohishi, K.; Maeda, Y.; Nakamura, N.; Endo, Y.; Fujita, T.; 7
A;Title: PIG-B, a membrane protein of the endoplasmic reticulum with a large lumenal dom A;Reference number: 871751; MUID:97015126; PMID:8861954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dolichyl-phosphate-mannose-glycolipid alpha-mannosyltransferase (EC 2.4.1.130) PIGB - ht N.Alternate names: membrane protein PIG-B; phosphatidyl-inositol glycolipid biosynthesis C;Species: Homo sapiens (man) C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Description: involved in surface protein binding to the membrane via glycosyl-phosphat by Pathway: GPI-anchor biosynthesis C,Reywords: glycosyltraneferase; hexosyltraneferase; transmembrane protein P;60-77/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                            Cjaccession: T51430
Rjato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.; Mew
submitted to the Protein Sequence Database, August 2000
A;Reference number: 225394
A;Accession: T51430
dolichyl-phosphate-mannose-glycolipid alpha-mannosyltransferase-like protein - Arabidope N;Alternate names: protein T913 150 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Best Local Similarity 83.3%; Pred. No. 28;
Matches 5; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Map position: 5
A;Introns: 78/2; 117/3; 152/3; 224/2; 318/2; 390/3; 441/2
A;Note: T9L3 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Cross-references: EMBL:AL391149
A,Experimental source: cultivar Columbia; BAC clone T9L3
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C;Species: Streptomyces viridochromogenes
C;Date: 31-Mar-1992 #sequence_revision 26-Apr-1996 #text_change 19-May-2000
C;Accession: S20686; PT0060
E;Alijah, R.; Hillemann, D.; Nussbaumer, B.; Pelzer, S.; Wohlleben, W.
Bubmitted to the EMBL Data Library, March 1997
A;Description: Gene disruption and gene replacement analysis of a 4 kb BamHI fragment of a 4 kb BamHI fragm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross.references: GB:AB003905; GB:AB003849; NID:g9105456; PIDN:AAF83407.1; GSPDB:GNO A;Experimental gource: strain 9a5c
A;Experimental gource: strain 9a5c
B;Simpson, A.JG; Reinard, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Canargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
Numbuited to GenBank, June 2000
A;Authors: Perreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fro J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laichado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D. A;Authors: da Silva, A.C.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, A.R.; Almeida, S.; Vettore, A.L.; A.R.Eference number: A59328
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A.Molecule type: DNA
A.Molecule type: DNA
A.Molecule type: DNA
A.Molecule type: DNA
A.Rosas.1-299 (ALI>
A.Crosa-references: EMBL:X65195, NID:g47997; PIDN:CAA46315.1; PID:g48001
R.Wohlleben, W.; Arnold, W.; Broer, I.; Hillemann, D.; Strauch, E.; Puehler, A.
Gene 70, 25-37, 1988
A;Title: Nucleoxide sequence of the phosphinothricin N-acetyltransferase gene from Stransference number: JT0409; MUID:89196914; PMID:3240868
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; WUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
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Pred. No. 16;
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Best Local Similarity 83.3%
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                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-218 <SIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28 LHOWHW 33
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A; Residues: 1-164 <WOH>
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C;Specias: Staphylococcus aureus
C;Specias: Staphylococcus aureus
C;Specias: Staphylococcus aureus
C;Specias: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: H90007
R;Kuroda, M.; Obta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
R;Kuroda, M.; Obta, T.; Uchiyama, I.; Baba, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1255-1240, 2001
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Retaus: preliminary
A
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C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C;Accession: A87628
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon, J.; Ernolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: A87628
A;Status: preliminary
A;Residues: 1-209 < STO-
A;Cossiues: 1-209 < STO-
A;Cossiues: Calcobacter Ca
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83.3%; Pred. No. 15;
tive 1; Mismatches 0; Indels
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Best Local Similarity 75.0°
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Matches 5; Conservative
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                                                                                                                                                                                                       306 HPWHWY 311
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                                                                               3 НКМНМУ 8
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C;Superfamily:
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A; Molecule type: DNA
A; Rosidues: 1-338, 'G', 340-348, 'S', 350-512 < GRA>
A; Rosidues: 1-338, 'G', 340-348, 'S', 350-512 < GRA>
A; Rosidues: 1-338, 'G', 340-348, 'S', 350-512 < GRA>
A; Rosidues: 1-338, 'G', 340-348, 'S', 350-512 < GRA>
A; Experimental source: NGTB 8061
B; Stephens, M.A.; Ortlepp, S.A.; Ollington, J.F.; McConnell, D.J.
J. Bacteriol. 158, '369-372, 1984
A; Title: Nucleotide sequence of the 5' region of the Bacillus licheniformis alpha-amylē
A; Accession: A91796
A; Mcestauce: 1-104 < STE>
A; Rosidues: 1-104 < STE>
A; Rossidues: 1-104 < STE>
A; Rossidues: 1-104 < STE>
A; Rossidues: 1-104 < STE
A; Title: Isolation and the 5'-end nucleotide sequence of Bacillus licheniformis alpha-a
A; Reference number: A21663; MUID:85076654; PMID:6334606
A; A; A; Title: Isolation and the S'-end nucleotide sequence of Bacillus licheniformis alpha-a
A; Reference number: A21663; MUID:85076654; PMID:6334606
A; Accession: A21663
A; Molecule type: DNA
A; Residues: 1-3', H', 5-12', P', 14-47', R', 49-61, 'V', 63, 'D', 65-67, 'VA', 70-71, 'S', 73-80, 'D', A; Residues: 1-3', H', 5-12', P', 14-47, 'R', 49-61, 'V', 63, 'D', 65-67, 'VA', 70-71, 'S', 73-80, 'D', A; Residues: 1-3', H', 5-12', P', 14-47, 'R', 49-61, 'V', 63, 'D', 65-67, 'VA', 70-71, 'S', 73-80, 'D', A; Residues: 1-3', H', 5-12', P', 14-47, 'R', 49-61, 'V', 63, 'D', 65-67, 'VA', 70-71, 'S', 73-80, 'D', A; Residues: 1-3', H', 5-12', P', 14-47, 'R', 49-61, 'V', 63, 'D', 65-67, 'VA', 70-71, 'S', 73-80, 'D', A; Residues: 1-3', H', 5-12', P', 14-47, 'R', 49-61, 'V', 63, 'D', 65-67, 'VA', 70-71, 'S', 73-80, 'D', A; Residues: 1-3', H', 5-12', P', 14-47, 'R', 49-61, 'V', 63, 'D', 65-67, 'VA', 70-71, 'S', 73-80, 'D', A; Residues: 1-3', H', 5-12', P', 14-47, 'R', 14-
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                                                                                                                                                                                                                                                                                                 .....ss-rererences: EMBL:U58762; NID:g1330398; PID:g1330400; PIDN:AAB00719.1; GSPDB:GN0
A;Experimental source: strain Bristol N2; clone T27F7
C;Genetics:
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A; Residues: 1-162, 'R', 164-512 < YUU>
A; Residues: 1-162, 'R', 164-512 < YUU>
A; Cross-references: GB: X30226; ND: G39551; PIDN: CAA26981.1; PID: G39552

A; Cross-references: ATCC 27811

B; Gray, G.L.; Mainzer, S.E.; Rey, M.W.; Lamsa, M.H.; Kindle, K.L.; Carmona, C.; Requadt J. Bacteriol. 166, 635-643, 1986

A; Title: Structural genes encoding the thermophilic alpha-amylases of Bacillus stearoth A; Reference number: A91817; MUID: 86195857; PMID: 3009417
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A;Title: Bacillus licheniformis alpha-amylase gene, amyL, is subject to promoter-indepe
A;Reference number: 139773; MUID:89213924; PMID:2540150
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submitted to the EMBL Data Library, May 1996
A; Description: The sequence of C. elegans cosmid T27F7.
A; Reference number: Z18613
A; Accession: T16945
                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DDB.
A;Residues: 1.283 cHAL>
A;Cross-references: EMBL:U58762; NID:91330398; PID:
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143 VHPWYWYI 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Map position: 2
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Matches
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C;Species Eurypelma californica
C;Species Eurypelma californica
C;Species Eurypelma californica
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 01-Aug-1997
C;Accession: A37975; 810606; 808108; 813440
J. Biol. Chem. 265, 1944-19452, 1950
J. Biol. Chem. 265, 1944-19452, 1950
A;Title: Arthropod hemocyanins. Molecular cloning and sequencing of cDNAs encoding the t
A;Reference number: A37975; MUID: 91060544; PMID: 2246235
A;Molecule type: mRNA
A;Residues: 1-631 < VOID.
A;Residues: 1-631 < VOID.
A;Residues: 1-631 < VOID.
A;Corss-references: EMBL: X16893
A;Note: 29-Ala was also found
R;Schartuu, W; Molecule type: Mr. Spiders, XXIII. Complete amino-acid sequence of subunit a of Bur
A;Note: 29-Ala was also found
R;Schartuu, W; MulD: 91025623; PMID: 2222854
A;Title: Hemocyanins in spiders, XXIII. Complete amino-acid sequence of subunit a of Bur
A;Reference number: 810606, MUID: 91025623; PMID: 2222854
A;Molecule type: protein
A;Residues: 2-29, A', 30-44, 'D', 46-132,'I', 134-148,'I', 150-154,'L', 156-262,'M', 264-411,'I
C;Superfamily: hemocyanin chain a #status experimental <MAT>
F;2-156/Domain: 1 < DOI>
F;2-156/Domain: 2 < DOI>
F;3-156/Domain: 2 < DOI>
F;3-157-800/Domain: 3 < DOI>
F;3-157-800/Domain: 3 < DOI>
F;3-157-179,206/Binding site: copper (His) #status predicted
F;2-6,330,366/Binding site: copper (His) #status predicted
M47031

bialaphos acetylhydrolase - Streptomyces hygroscopicus
bialaphos acetylhydrolase - Streptomyces hygroscopicus
c;Species: Streptomyces hygroscopicus
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 17-Mar-2000
C;Accession: A47031
R;Raibaud, A.; Zalacain, M.; Holt, T.G.; Tizard, R.; Thompson, C.J.
J. Bacteriol. 173, 4454-4463, 1991
A;Title: Nucleotide sequence analysis reveals linked N-acetyl hydrolase, thioesterase,
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T1645
hypothetical protein T27F7.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Dete: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T16945
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A; Residues: 1-299 <RAI>
A; Note: sequence extracted from NCBI backbone (NCBIN:41300, NCBIP:41303)
C; Superfamily: probable lipolytic protein ybac
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Pred. No. 44;
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                                                                                                                                                                                                                                                                                                                                                                                             .
A;Reference number: A47031; MUID:91294191; PMID:2066341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5;
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Pred. No. 21;
0; Mismatches
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1; Mismatches
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5; Conservative
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Best Local Similarity 83...
5; Conservative
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary
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A;Cross-references: EMBL:X16650; NID:g9249; PIDN:CAA34643.1; PID:g829205
R;Voll, W.; Voit, R.
R;Voll, M.; Voit, R.
A;Title: Natl. Acad. Sci. U.S.A. 87, 5312-5316, 1990
A;Title: Characterization of the gene encoding the hemocyanin subunit e from the tarant A;Reference number: A35772; MUID:90319102; PMID:2371273
A;Cross-references: GB:JO1542; GB:JO1543; GB:M12033; GB:M12034; NID:g142428; PIDN:AAA2: R;Chung, H.S.; Friedberg, F. Biochem. J. 185, 387-395, 1980
A;Title: Sequence of the N-terminal half of Bacillus amyloliquefaciens alpha-amylase. A;Reference number: A90307; MUID:80241725; PMID:6156671
                                                                                                                                                                                                                                                                 A;Molecule type: protein
A;Residues: 33-53,'I',55-63,'L',65-78,'D',80-83,'S',85-222 <CHU>
R;Palva, I.; Pettersson, R.F.; Kalkkinen, N.; Lehtovaara, P.; Sarvas, M.; Soderlund, H
R;Palva, I.; Pettersson, R.F.; Kalkkinen, N.; Lehtovaara, P.; Sarvas, M.; Soderlund, H
A;Palva, I.; Pettersson, R.F.; Kalkkinen, N.; Lehtovaara, P.; Sarvas, M.; Soderlund, H
A;Title: Nucleotide sequence of the promoter and NH2-terminal signal peptide region of
A;Reference number: 139756; MUID:82051296; PMID:6170539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Biol. Chem. 265, 19447-19452, 1990
A;Title: Arthropod hemocyanins. Molecular cloning and sequencing of cDNAs encoding the A;Reference number: A37975; MUID:91060544; PMID:2246235
A;Accession: S13441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A Pathway: glycogen/starch degradation
C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
C;Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
F;1-31/Domain: signal sequence #status predicted <BIO>
F;32-514/Product: alpha-amylase #status predicted <MPT>
F;229-352/Domain: alpha-amylase core homology <AMY>
F;133,231,266/Binding site: calcium (Asn, Asp, His) #status predicted
F;262,292,359/Active site: Asp, Glu, Asp #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A, Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hemocyanin chain e - American tarantula (Burypelma californica)
C;Species: Burypelma californica
C;Date: 15-Nov-1984 #sequence revision 31-Mar-1992 #text_change 22-Jun-1999
C;Accession: S06701; A35772; Š13441; A02566; A24179; B37975; S08107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:M18424; NID:g142430; PIDN:AAA22192.1; PID:g142431 C;Function:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA
A;Residues: 1-39 <RE2>
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best Local Similarity 100.0%; Pred. No. 51;
Best Local Similarity 00.0%; Mismatches
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A;Reference number: S06701
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A; Residues: 1-64;604-624 <VOL2>
R; Voit, R; Feldmaier-Fuchs, G.
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A; Residues: 1-624 <VOI>
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A; Molecule typee DNA
A; Mosiduse typee DNA
A; Mosiduse typee DNA
A; Mosiduse typee DNA
A; Mosiduse typee DNA
A; Cross-references: GB:M65637; NID:g142498; PIDN:AMA22232.1; PID:g142499
R; MAD, H; Fittack, P. P.; Lampen, J.O.
J. Bacteriol. 149, 372-373, 1982
A; Mitte: N-Verminal amino acid sequence of Bacillus litcheniformis alpha-amylase: comparing the momber: A26151; MUD:82098050; PMID:6172418
A; Accession: A661919
A; Rocession: A61919
A; Rocession
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N'Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C;Species: Bacillus amyloliquefaciens
C;Species: Bacillus amyloliquefaciens
C;Accession: A92389; A90307; Ī39756; I39763; A00843
R;Takkinen, K.; Pettersson, R.F.; Kalkkinen, N.; Palva, I.; Soderlund, H.; Kaariainen, I. Biol. Chem. 258, 1007-1013, 1983
A;Title: Amino acid sequence of alpha-amylase from Bacillus amyloliquefaciens deduced fr A;Reference number: A92389; MUID:83108808; PMID:6185474
                                 A; Molecule type: DNA
A; Residues: 1-29 < LAO>
A; Table: 1. PID: GSIMZ6412; NID: G341477; PIDN: AAA22237.1; PID: GS16590
B; Jordensen, P.L.; Hansen, C.K.; Poulsen, G.B.; Diderichsen, B.
Gene 96, 37-41, 1990
A; Title: In vivo genetic engineering: homologous recombination as a tool for plasmid con A; Reference number: 139772; MUID: 91092499; PMID: 2265757
A; Accession: 139772
A; Status: translated from GB/EMBL/DDBJ
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Best Local Similarity
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A;Molecule type: DNA
A;Residues: 1-514 <TAK>
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Gaps

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A/Cross-references: EMBL:X16894; NID:99268; FIDN:CAA34772.1; PID:99269
R/Schneider, H.J.; Drexel, R.; Feldmaier, G.; Linzen, B.; Lottspeich, F.; Henschen, A. Hoppe-Seyler's Z. Physiol. Chem. 364, 135-1381, 1983
A/Title: Hemocyanins in solders, X111[81]. Complete amino-acid sequence of subunit e from A; Reference number: A02566; MUID:84059635; PMID:6357986
AAccession: A02566
AAmolecule type: protein
A; Residues: 2-29, R', 31-46, D', 48-79, K', 81-90, H', 92-110, 112-159, K', 161-216, H', 218-25
C; Senetics:
A/Introns: 65/1; 137/3; 206/2; 338/3; 381/3; 426/3; 489/1; 560/3
C; Superfamily: hemocyanin
C; Reywords: copper; hemocyanin c #status experimental <AT>F; 2-634 Product: hemocyanin chain e #status experimental <AT>F; 2-150/Domain: 1 < D01>F; 2-150/Domain: 3 < D02>F; 375-624/Domain: 3 < D02>F; 372-624/Domain: 3 < D03>F; 372-624/Domain: 3 < D03>F;
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Search completed: December 16, 2003, 14:19:17 Job time: 11.3333 secs

3 HKWHWYV 9 | |||:: 168 HHWHWHI 174

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RA Kunst F., Ogasawara N., Moszar I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Brouillet S., Bruschic L., Brans A., Braun M., Brighell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Coldwell B., Capuano V., Carter N.M.,
RA Brouillet S., Brington J., Fabret C., Fertrai E., Foulger D.,
RA Britz C., Fujita M., Pujita Y., Fuma S., Galizzi A., Galleron N.,
RA Entian K.D., Brrington J., Fabret C., Fertrai E., Foulger D.,
RA Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
Antibert H., Holsappel S., Hosono S., Willo M.F., Itaya M., Jones L.,
Arobyashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
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RA Mutia K., Laylue A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Baco M., Rivolte C., Rocha E., Roche B., Rose M., Sadaie Y.,
Sekiguchi J., Sekowska A., Seros S.J., Serror P., Shin B.S., Soldo B.,
RA Borokin A., Tamakoshi A., Tanahaka T., Tarkamaru K.,
Tokasarotti A., Tanakoshi A., Taramaka T., Tarkamaru K.,
Tokasarotti A., Tanakoshi A., Tanaka T., Tarkamaru K.,
Tokasarotti A., Tosaconi E., Tarkai T., Tarkamaru K.,
Tokasarotti A., Tosaconi A., Taramaka T., Tarkamaru K.,
Tokasarotti A., Tanakoshi A., Tanakoshi A., Tarkamaru K.,
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Tokasarotti A., Tanakoshi A., Tanakoshi A., Tarkamaru K.,
Tokasarotti A., Tarkamaru K., Tanakoshi A., Tanakoshi A., Tarkamaru K.,
Tokasarotti A., Tarkamaru K., Tarkamaru K
                                        Q9muy9 poa pratens
Q10295 schizosacch
P32791 saccharomyc
Q8xLp0 erysiphe gr
Q9c169 neurospora
P42512 pseudomonas
Q63177 rattus norv
Q54782 mus musculu
Q92972 chlamydia p
               odontella s
phleum prat
 halorubrum
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MEDALINE-98015415; PubMed=9353931;
Medina N., Vannier F., Roche B., Autret S., Levine A., Seror S.J.;
"Sequencing of regions downstream of adda (98 degrees) and citG (289 degrees) in Bacillus subtilis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         characterization of two genes differentially repressed by metal
093742
               P49833
                               Q9muz4
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NCBL_TaxID=1423;
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                                                                                                                                                                                                                                                                                                             01-OCT-1994 (Rel. 30, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 41, Last annotation update)
Metalloregulation DNA-binding stress protein.
                                                      PAP SCHPO
FREI YEAST
CATA ERYGR
CAT3 NEUCR
FPTA PSEAE
                             MATK PHLPR
MATK POAPR
                                                                                                                                                M2B2_MOUSE
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MEDLINE=98044033; PubMed=9384377;
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                                                                                                                                                                                                                                                                                                                                                                                     Bacillus subtilis.
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AC P37960;
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74.689 Million cell updates/sec
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                                                                                                     December 16, 2003, 14:06:35 ; Search time 5.66667 Seconds
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Q9nf15
P22383
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P16665
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Q9n2d1
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              GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                    127863 seqs, 47026705 residues
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HCYC EURCA
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AMY BACAM
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TRYT_PIG
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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us-09-870-089b-9.rsp

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Viari A., Wambutt R., Wedler B., Wedler H., Weitzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.; "The complete genome sequence of the Gram-positive bacterium Bacillus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OXIDATIVE KILLING.
INDUCTION: BY OXIDATIVE STRESS AND BY GROWTH IN MINIMAL MEDIUM
LACKING IRON (FE-III), OR ONE OF THE DIVALENT CATIONS MANGANESE.
                                                                                                                                                                                                                                                                                                                                                                                                                               Chen L., Helmann J.D.;
"Bacillus subtilis MrgA is a Dps(PexB) homologue: evidence for
metalloregulation of an oxidative-stress gene.";
Moi. Microbiol. 18:295-3078.
-!- FUNCTION: FORMS HIGHLY STABLE, MULTIMERIC PROTEIN-DNA COMPLEXES
WHICH ACCUMULATE IN STATIONARY-PHASE CELLS AND PROTECT AGAINST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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15-UUL-1998 (Rel. 35, Last sequence update)
28-FRB-2003 (Rel. 41, Last amocation update)
General stress protein 20U (GSP20U) (DPS protein homolog).
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NCBI_TaxID=1423;
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153 AA; 17332 MW; 3082CF803401E17D CRC64;
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MEDLINE=96296451; PubMed=8709848;
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EMBL; Z22928; CAA80510.1; -.
EMBL; Z93941; CAEN0790.1; -.
EMBL; Z93120; CAEN5288.1; -.
PIR, G69660; G69660.
Subtilist; BG10864; mrgA.
InterPro; IPR001217; DPS.
InterPro; IPR001519; Ferritin.
Pfam; PF00210; ferritin; 1.
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ProDom; PD149803; DPS; 1.
PROSITE; PS00818; DPS 1; 1.
PROSITE; PS00819; DPS_2; 1.
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les 6, Conservative
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ID G20U BACSU
AC P80879;
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                                                                                                                                                            RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R. Boursier L., Brans A., Braun M., Brighell S.C., Bron S.,
RA Borriss R. Boursier L., Brans A., Braun M., Brighell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Brouillet S., Brington J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizor F., Devine K.M., Duscerhoff A., Erlrich S.D., Emmerson P.T.,
RA Brita C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Guiseppi G., Guy B.J., Haga K., Haicch J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M., Itaya M., Jones L.,
RA McDissephi G., Guy B.J., Haga K., Haicch J., Barrwood C.R., Henaut A.,
RA Korita K., Lapidus A., Liu H., Masuda S., Maulo M., Klein C.,
RA Medina N., Mellado R.P., Mizuno M., Mosetl D., Nakai S., Runano M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Takeuchi M., Tamakoshi A., Taranier E., Schleich S., Schroeter R., Vastumoto K., Yata K.,
RA Tosaco V., Uchiyama S., Vandelber M., Vannier F., Vastumoto K., Yata K.,
RA Tosaco V., Uchiyama S., Vandelber M., Vannier F., Vastumoto K., Yata K.,
RA The complete genome sequence of the Gram-positive bacterium Bacillus
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "First steps from a two-dimensional protein index towards a response-
regulation map for Bacillus subtilis.";
Electrophoresis 18:1451-1463(1997).
-!- INDUCTION: BY HEAT SHOCK, SALT STRESS, OXIDATIVE STRESS, GLUCOSE
LIMITATION AND OXYGEN LIMITATION.
-!- SIMILARITY: BELONGS TO THE DPS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-97443988; PubMed-9298659;
Antelmann H., Bernhardt J., Schmid R., Mach H., Voelker U.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    144 AA; 16462 MW; 21ADBC4438E5E3E2 CRC64;
                                                                                                                                                MEDLINE=98044033; PubMed=9384377;
Microbiology 143:3431-3441(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF008220; AAC00237.1; -.
EMBL; 299119; CAB15043.1; -.
PIR; H69618; H69618.
Subtilist; BG12584; dps.
InterPro; IPR002177; Dps.
InterPro; IPR00119; Ferritin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Heat shock; Complete proteome.
INIT MET 0 0
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ProDom; PD149803; DP5; 1.
PROSITE; PS00818; DP5 1; 1.
PROSITE; PS00819; DP5-2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=168 / IS58;
                                                                          SEQUENCE FROM N.A.
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   SOLUMENT TO BE SEED TO COURT OF SEED THE SEED TH
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68.8%; Score 44; DB 1; Length 144;

Query Match

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SUBFAMILY.
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P14750;
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                                                                                                                                                                            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67.2%; Score 43; DB 1; Length 299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
          1; Indels
                                                                                                                                                                                                                                                                                                       BIALAPHOS AS ONE OF THE FINAL STEPS OF THE BIALAPHOS BIOSYNTHETIC PATHWAY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4265C8E6E10FAE97 CRC64;
                                                                                                                                                                                  Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                01-APR-1993 (Rel. 25, Created)
01-FFB-1996 (Rel. 33, Last sequence update)
08-FBB-2003 (Rel. 41, Last annotation update)
Acetyl-hydrolase (EC 3.1.1.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hemocyanin C chain (HcC).
75.0%; Pred. No. 4.5; tive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match billerity 83.3%; Pred. No. 12; Best Local Similarity 83.3%; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eurypelma californica (American tarantula).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, M64783, AAA79277.1; -.
InterPro, IPR002168; Lipolytic_enzyme.
InterPro, IPR000379; Ser_effrs site.
PROSITE, PS01173; LIPASE_GDXG_SER; 1.
PROSITE; PS01174; LIPASE_GDXG_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydrolase; Antibiotic biosynthesis.
ACT SITE 73 POTENTI
ACT SITE 143 143 POTENTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                299 AA; 32096 MW;
                                                                                                                                                                   Streptomyces hygroscopicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
           6; Conservative
                                                                                                STANDARD;
                                        22 LHNYHWYV 29
 Best Local Similarity
                             2 LHKWHWYV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              267 HVWHWY 272
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Q9NFL6;
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                                                                                                                                                                                                            Voit R., Feldmaler-Puchs G., Schweikardt T., Decker H., Burmester T.; "Complete sequence of the 24-mer hemocyanin of the tarantula Burypelma californicum. Structure and intramolecular evolution of the
                                                                                                                                                                                                                                                                                                                                J. Biol. Chem. 275:39339-39344 (2000).
-!- FUNCTION: HEMOCYANINS ARE COPPER-CONTAINING OXYGEN CARRIERS OCCURRING FREELY DISSOLVED IN THE HEMOLYMPH OF MANY MOLLUSKS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBDIT: TRRANTULA HEMOCYANIN IS A 24-CHAIN POLYMER WITH SEVEN DIFFERENT CHAINS IDENTIFIED.
-!- SUBCELLULAR LOCATION: Extracellular.
-!- TISSUE SPECIFICITY: Hemolymph.
-!- MISCELLANEOUS: THE TWO COPPER IONS BOUND EACH HAVE 3 NITROGEN LIGANDS (PRESUMALLY CONTRIBUTED BY HIS RESIDUES) AND SHARE A BRIDGING LIGAND (POSSIBLY CONTRIBUTED BY A TYR RESIDUE) IN ADDITION TO BINDING OXYGEN.
-!- SIMILARITY: BELONGS TO THE TYROSINASE FAMILY. HEMOCYANIN
Eukaryota, Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
Mygalomorphae; Theraphosidae; Aphonopelma.
NCBI_TaxID=29932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
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BY SIMILARITY.
BY SIMILARITY.
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COPPER 1 (BY SIMILARITY).
COPPER 2 (BY SIMILARITY).
COPPER 2 (BY SIMILARITY).
COPPER 2 (BY SIMILARITY).
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1; Mismatches
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InterPro; IPR005203; hemocyanin C.
InterPro; IPR005204; hemocyanin N.
InterPro; IPR00227; Tyrosinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00209; HEMOCYANIN 1; 1. PROSITE; PS00210; HEMOCYANIN 2; 1. PROSITE; PS00498; TYROSINASE 2; 1.
                                                                                                                                                                                    MEDLINE=20564303; PubMed=10961996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00372; hemocyanin; 1.
Pfam; PF03723; hemocyanin C; 1.
Pfam; PF03722; hemocyanin N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AJ277489; CAB89495.1; -.
HSSP; P04253; 1LLA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   584
174
178
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Matches 5: Conserv
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INIT MET 0
DISULFID 536
                                                                                                                                SEQUENCE FROM N.A.
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Gaps

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Indels

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Pred. No. 24; 1; Mismatches

71.48;

Best Local Similarity

Conservative

5,

Matches

3 HKWHWYV 9 | |||:| 173 HHWHWHV 179

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=91025623; PubMed=2222854; Schartau W., Merzger W., Sonner P., Geisert H., Storz H.; Schartau W., Merzger W., Sonner P., Geisert H., Storz H.; "Hemocyanins in spiders, XXIII. Complete amino-acid sequence of subunit a of Eurypelma californicum hemocyanin."; Biol. Chem. Hoppe-Seyler 371:557-565[1990].

-i. FUNCTION: HEMOCYANINS ARE COPPER-CONFAINING OXYGEN CARRIERS OCCURRING FREELY DISSOLVED IN THE HEMOLYMPH OF MANY MOLLUSKS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1. SUBCRIT: TARANTULA HEMOCYANIN IS A 24-CHAIN POLYMER WITH SEVEN DIFFERENT CHAINS IDENTIFIED.
-1. SUBCRITIOLAR LOCATION: Extracellular.
-1. TISSUB SPECITY: Hemolymnh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE SPECIFICITY: Hemolymph.

MISCELLANEOUS: THE TWO COPPER IONS BOUND EACH HAVE 3 NITROGEN LIGANDS (PERSUMABLY CONTRIBUTED BY HIS RESIDUES) AND SHARE A BRIDGING LIGAND (POSSIBLY CONTRIBUTED BY A TYR RESIDUE) IN ADDITION TO BINDING OXYGEN.

SIMILARITY: BELONGS TO THE TYROSINASE FAMILY. HEMOCYANIN
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COPPER 2 (PROBABLE).
COPPER 2 (PROBABLE).
COPPER 2 (PROBABLE).
COPPER 2 (PROBABLE).
BY SIMILARITY.
N-LINKED (GLCNAC. . . ) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                           Voit R., Feldmaier-Fuchs G.; "Arthropod hemocyanins Molecular cloning and sequencing of cDNAs encoding the tarantula hemocyanin subunits a and e."; J. Biol. Chem. 265:19447-19452(1990).
                                                                                                            Burypelma californica (American tarantula).
Bukaryota, Metazoa, Arthropoda, Chelicerata, Arachnida, Araneae,
Mygalomorphae, Theraphosidae, Aphonopelma.
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PROSITE; PS00210; HEMOCYANIN_2; 1.
PROSITE; PS00498; TYROSINASE 2; 1.
Transport; Oxygen transport; Copper; Glycoprotein; Hemolymph.
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01-NOV-1990 (Rel. 16, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000896; Hemocyanin.
InterPro; IPR005203; hemocyanin_C.
InterPro; IPR005204; hemocyanin_N.
InterPro; IPR005227; Tyrosinase.
Pfam; PF00372; hemocyanin; 1.
Pfam; PF03723; hemocyanin; 1.
Pfam; PF03722; hemocyanin; 1.
Pfam; PF03722; hemocyanin, N; 1.
PRINTS; PR00187; HAEMOCYANIN.
                                                                                                                                                                                                                                                                                                             MEDLINE=91060544; PubMed=2246235;
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HSSP; P04253; 1LLA.
                                                      Hemocyanin A chain (HcA).
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                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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Score 43; DB 1; Length 630;

67.2%;

Query Match

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STRAIN=AICC 27811;
MEDLINE=86111694; PubMed=2418011;
Yuuki T., Nomura T., Tezuka H., Tsuboi A., Yamagata H.,
Yuuki T., Nomura T., Tezuka S.;
"Complete nucleotide sequence of a gene coding for heat- and
pH-stable alpha-amylase of Bacillus licheniformis: comparison of the
amino acid sequences of three bacterial liquefying alpha-amylases
deduced from the DNA sequences.";
J. Blochem. 98:1147-1156(1985).
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MEDLINE-89213924; PubMed=2540150;
Laoide B.M., Chambliss G.H., McConnell D.J.;
"Bacillus licheniformis alpha-amylase gene, amyL, is subject to promoter-independent catabolite repression in Bacillus subtilis.";
J. Bacteriol. 171:2435-2442(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gray G.L., Mainzer S.E., Rey M.W., Lamsa M.H., Kindle K.L., Carmona C., Requadt C.;
"Structural genes encoding the thermophilic alpha-amylases of Bacillus stearchermophilus and Bacillus licheniformis.";
J. Bacteriol. 166:635-643(1986).
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MEDIJURE-82098050 P. P., Lampen J.O.;

Kuhn H., Fieterzek P.P., Lampen J.O.;

"N-terminal amino acid sequence of Bacillus licheniformis
                                                                                         01-JAN-1988 (Rel. 06, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Alpha-amylase precursor (BC 3.2.1.1) (1,4-alpha-D-glucan
                                                                                                                                                                                                                                                      Bacillus licheniformis.
Bacteria, Firmicutes; Bacillales; Bacillaceae, Bacillus.
512 AA.
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MEDLINE=86195857; PubMed=3009417;
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                                                                 01-JAN-1988 (Rel. 06, Created)
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   STANDARD;
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AMY BACLI
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                                                                                                                                                                                                                                                                                  PRINTS; PRO0110; ALPHAAMYLASE.
SWART; SM00642; Aamy; 1.
Hydrolase; Glycosidase; Carbohydrate metabolism; Signal; 3D-structure.
SIGNAL
               NOVOZYMĖS.
MISCELLANBOUS: ABLE TO WORK AT RELATIVELY HIGH (ALKALINE) PH
VALUES (UP TO PH 11) AND AT HIGH TEMPERATURES (UP TO 100 DEGREE
                                           SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
liquefaction of starch-containing mashes and in the detergent industry to remove starch. Sold under the name Termamyl by
                                                                                                                                                                                                                                                                                                                                                   9999
                                                                                                                                                                                                                                                                                                                  ALPHA-AMYLASE.
BY SIMILARITY.
BY SIMILARITY.
C -> Y (IN REF. 5
R -> L (IN REF. 5
S -> G (IN REF. 2
S -> G (IN REF. 2
                                                                                                                                EMBL; X03236; CAA26981.1; ---
EMBL; M38570; AAA22226.1; ---
EMBL; M38570; AAA22226.1; ---
EMBL; K01984; AAA22240.1; ---
EMBL; RA9193.1; ---
EMBL; A1930; CAA01355.1; ---
EMBL; A2193; ALBSL.
PDB; 1BPL; 17-AUG-96.
PDB; 1BA2; 21-UN-01.
PDB; 1E3X; 21-UN-01.
PDB; 1E3X; 21-UN-01.
PDB; 1E43; 21-UN-01.
PDB; 1C80; 30-JAN-03.
InterPro; IPR0066589; Alpa amyl cat sub.
InterPro; IPR006689; Alpa amyl cat.
InterPro; IPR006047; Alpha amyl cat.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AMY BACAM STANDARD, PRT; 514 AA.
PD0692,
21-JUL-1986 (Rel. 01, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
16-SEP-2003 (Rel. 42, Last annotation update
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Bust Local Similarity 100.00
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512 AA;
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SIGNAL
                                                                                                                "Amino acid sequence of alpha-amylase from Bacillus amyloliquefaciens deduced from the nucleotide sequence of the cloned gene."; J. Biol. Chem. 258:1007-1013(1983).
                                                                                                                                                                                         SEQUENCE OF 32-222.
MEDLINE-80241725; PubMed=6156671;
"Chung H.S., Friedberg F."
"Sequence of the N-terminal half of Bacillus amyloliquefaciens alpha-
                                                                                                                                                                                                                                                                                                                        MEDIJUE-82051296; PubMed-6170539; Palva I., Pettersson R.F., Kalkkinen N., Lehtovaara P., Sarvas M., Soederlund H., Takkinen K., Kaeaeriaeinen L.; "Nucleotide sequence of the promoter and NH2-terminal signal peptide region of the alpha-amylase gene from Bacillus amyloliquefaciens."; Gene 15:43-51(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-39 FROM N.A.
MEDLINE=88137952; PubWed=2230166;
Ruchonen L., Hackman P., Lehtcovaara P., Knowles J.K.C., Karaenen S.;
"Efficient secretion of Bacillus amyloliquefaciens alpha-amylase by its own signal peptide from Saccharomyces cerevisiae host cells.";
Gene 59:161-170(1987).
                                                              MEDLINE-B3108808; PubMed-6185474;
Takkinen K., Pettersson R.F., Kalkkinen N., Palva I., Soederlund H.,
Kaeaeriaeinen L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosacharides and polysaccharides. SUBCELLULAR LOCATION: SECTEDEd. SECTION: SECTION: SECTION: SECTION: SECTION: SECTION: MANILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY:
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L -> 1 (IN REF. 2).

I -> 5 (IN REF. 2).

G -> 5 (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interpro; IPR006589; Alp amyl_cat_sub.
Interpro; IPR0066047; Alpha amyl_cat.
Pfam; PF00128; alpha-amylase; 1.
SMART; SM00642; Aamy; 1.
                                                                                                                                                                                                                                                                              3iochem. J. 185:387-395(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58403 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, J01542; AAA22191.1; -.
EMBL, V00092; CAA23430.1; -.
EMBL, AZ0154; CAA01489.1; -.
EMBL, M18424; AAA22192.1; -.
                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-96 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PDB, 1E3X; 21-JUN-01.
PDB, 1E3Z; 21-JUN-01.
PDB, 1E40; 21-JUN-01.
PDB, 1E43; 21-JUN-01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            514 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; A92389; ALBSN.
                                      SEQUENCE FROM N.A.
   NCBI TaxID=1390;
                                                                                                                                                                                                                                                                 amylase.";
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Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VO11 W., Voit R., "Characterization of the gene encoding the hemocyanin subunit e from "Characterization of the gene encoding the hemocyanin subunit e from ".".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleotide sequence corresponding to subunit e.";

Bur. J. Biochem. 159:23-29 (1986)

-i- FUNCTION: HEMOCYANINS ARE COPER-CONTAINING OXYGEN CARRIERS

OCCURRING PREELY DISSOLVED IN THE HEMOLYMPH OF MANY MOLLUSKS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-84059635; PubMed=6357986;
Schneider H.-J., Drexel R., Feldmaier G., Linzen B., Lottspeich F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBUNT: TARANTULA HEMOCYANIN IS A 24-CHAIN POLYMER WITH SEVEN DIFFERENT CHAINS IDENTIFIED.
-!- SUBCELLULAR LOCATION: Extracellular.
-!- TISSUE SPECIFICITY: HEMOLYMPh.
-!- MISCELLANEOUS: THE TWO COPPER IONS BOUND EACH HAVE 3 NITROGEN LIGANDS (PRESIDURE) CONTRIBUTED BY HIS RESIDUES) AND SHARE A BRIDGING LIGAND (POSSIBLY CONTRIBUTED BY A TYR RESIDUE) IN ADDITION TO BINDING OXYGEN.
-!- SIMILARITY: BELONGS TO THE TYROSINASE FAMILY. HEMOCYANIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 74-599 FROM N.A.
MEDLINE-86300721; PubMed=3017715;
Voit R., Schneider H.-J.;
"Tarantula hemocyanin mRNA. In vitro translation, cDNA cloning and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Voit R., Feldmaier-Fuchs G.;
"Arthropod hemocyanins. Molecular cloning and sequencing of cDNAs encoding the tarantula hemocyanin subunits a and e.";
J. Biol. Chem. 265:19447-19452 (1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Burypelma californica (American tarantula).
Bukaryota, Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
Mygalomorphae; Theraphosidae; Aphonopelma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Henschen A.; "Hemcyanins in Spiders, XVIII. Complete amino-acid sequence of subunit e from Eurypelma californicum hemocyanin."; Hoppe-Seyler's Z. Physiol. Chem. 364:1357-1381(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the tarantula Eurypelma californicum.";
Proc. Natl. Acad. Sci. U.S.A. 87:5312-5316(1990).
                                                                                                                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Created)
01-APR-1990 (Rel. 14, Last sequence update)
28-FBR-2003 (Rel. 41, Last annotation update)
Hemocyanin E chain (HCE).
                                                                                                                                                                                                                                                           623 AA.
                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=90319102; PubMed=2371273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=91060544; PubMed=2246235;
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                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                         183 KWHWY 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MCBI_TaxID=29932;
4 KWHWY 8
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                                                                                                                                                                                                                                                           HCYE EURCA
                                                                                                                                                                                                                                                                                             DESCRIPTION OF COURT AND THE SET TO THE SET
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TISSUE=Heart;
MEDLINE=205643103; PubMed=10961996;
Woit R., Feldmaier-Fuchs G., Schweikardt T., Decker H., Burmester T.;
"Complete sequence of the 24-mer hemocyanin of the tarantula Eurypelma californicum. Structure and intramolecular evolution of the
                                                                                               -1- SUBUNIT: SCORPION HEMOCYANIN IS A 24-CHAIN POLYMER WITH 8
DIFFERRY CHAINS IDENTIFIED, ASSEMBLED IN HEXAMERIC SUBSTRUCTURES.
-1- SUBCELLULAR LOCATION: Extracellular.
-1- TISSUB SPECIFICITY: Hemolymph.
-1- PTM: THREE DISULFIDE BONDS ARE PRESENT.
-1- MASS SPECIROMETRY: MW-71890; MW ERR-7; METHOD=Electrospray.
-1- MASS SPECIROMETRY: MW-71890; MW ERR-7; METHOD=Electrospray.
-1- LIGANDS (PRESUMABLY COMPRIBUTED BY HIS RESIDUES) AND SHARE A BRIDGING LIGAND (POSSIBLY CONTRIBUTED BY A TYR RESIDUE) IN ADDITION TO BINDING OXYOSN.
-1- STMILARITY: BELONGS TO THE TYROSINASE FAMILY. HEMOCYANIN
                                        Bur. J. Biochem. 233:93-101(1995).
-1- FUNCTION: HEMOCYANINS ARE COPPER-CONTAINING OXYGEN CARRIERS OCCURRING FREELY DISSOLVED IN THE HEMOLYMPH OF MANY MOLLUSKS AND
"Complete amino acid sequence of the Aa6 subunit of the scorpion
Androctonus australis hemocyanin determined by Edman degradation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eurypelma californica (American tarantula).
Eukaryota, Metazoa, Arthropoda, Chelicerata, Arachnida, Araneae,
Mygalomorphae, Theraphosidae, Aphonopelma.
MCBI_TaxID=29932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       170 COPPER 1 (PROBABLE).
174 COPPER 1 (PROBABLE).
201 COPPER 2 (PROBABLE).
321 COPPER 2 (PROBABLE).
325 COPPER 2 (PROBABLE).
374 PHOCSPHORYLATION (PROBABLE).
374 PHOCSPHORYLATION (PROBABLE).
71785 MW, E788136AE3DEPODZ CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 42; DB 1; Length 626;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                          PIR; SG7964; BIR; SG7964.
HSSP; P04253; 10XY.
InterPro; IPR000896; Hemocyanin.
InterPro; IPR000503; hemocyanin.
InterPro; IPR005204; hemocyanin.
InterPro; IPR005204; hemocyanin.
InterPro; IPR005207; Tyrosinase.
Pfam; PF03722; hemocyanin.; 1.
Pfam; PF03722; hemocyanin.; 1.
Pfam; PF03722; hemocyanin. N; 1.
PROSITE; PS00209; HEMOCYANIN.; 1.
PROSITE; PS00210; HEMOCYANIN.; 1.
PROSITE; PS00210; HEMOCYANIN.; 1.
PROSITE; PS00498; TYROSINASE_2; 1.
Transport; Oxygen transport; Copper; Hemolymph; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hemocyanin F chain (HcF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65.6%; Score 42,
57.1%; Pred. No. 33;
tive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 628 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 57.1.
Local 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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169 HHWHWHI 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   201
321
321
325
361
374
374
                               mass spectrometry."
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                                                                                          ARTHROPODS.
                                                                                                                                                                                                                                                                     SUBFAMILY.
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HCYF_EURCA
ID HCYF_EURCA
AC Q9NFL5;
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SEQUENCE
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Eukaryota, Metazoa, Arthropoda; Chelicerata, Arachnida; Scorpiones;

Buthoidea; Buthidae; Androctonus.
                                                                                                                                      R InterPro; IPR005203; hemocyanin.
R InterPro; IPR005203; hemocyanin.
R InterPro; IPR005203; hemocyanin.C.
R InterPro; IPR005227; Tyrosinase.
R Pfam; PF03723; hemocyanin; 1.
R PROSITE; PS00210; HEMOCYANIN 2; 1.
R PROSITE; PS00210; HEMOCYANIN 2; 1.
R PROSITE; PS00499; TYROSINASE_2; 1.
R Transport; Oxygen transport; Copper; Glycoprotein; Hemolymph.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         M -> M (IN REF. 2).
C -> D (IN REF. 2).
R -> K (IN REF. 2).
A -> H (IN REF. 2).
K -> R (IN REF. 2).
K -> H (IN REF. 2).
H -> M (IN REF. 2).
C -> H (IN REF. 2).
C -> M (IN REF. 2).
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BUDLINE=56061336; PubMed=7588779;
BUZY A., Gagnon d., Lamy J., Thibault P., Forest E.,
Hudry-Clergeon G.;
                                                                                                                                                                                                                                                                                                                                        COPPER 1 (PROBABLE).
COPPER 1 (PROBABLE).
COPPER 2 (PROBABLE).
COPPER 2 (PROBABLE).
COPPER 2 (PROBABLE).
BY SIMILARITY.
N-LINKED (GLCNAC...)
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COPPER 1 (PROBABLE).
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V -> P (IN REF. 3).
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01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
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 EMBL; X16650; CAA34643.1; --.
EMBL; X16651; CAA34643.1; JOINED.
EMBL; X16652; CAA34643.1; JOINED.
EMBL; X16653; CAA34643.1; JOINED.
EMBL; X16654; CAA34643.1; JOINED.
EMBL; X16656; CAA34643.1; JOINED.
EMBL; X16656; CAA34643.1; JOINED.
EMBL; X16657; CAA34643.1; JOINED.
PIR; S06701; BHTLE.
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623 AA;
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1199
3319
3323
3528
444
46
79
110
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P80476;
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DISULFID
CARBOHYD
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CONFLICT
CONFLICT
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HCY6_ANDAU
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Gaps

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MEDLINE=90015168; PubMed=2797181;
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                                                   African mandrill
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HUMAN
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PAR3 HUMAN
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à
                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entilies requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Biol, Chem. 275:39339-39344 (2000).
FUNCTION: HEMOCYANINS ARE COPPER-CONTAINING OXYGEN CARRIERS OCCURRING FREELY DISSOLVED IN THE HEMOLYMPH OF MANY MOLLUSKS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COPPER 1 (BY SIMILARITY).
COPPER 1 (BY SIMILARITY).
COPPER 1 (BY SIMILARITY).
COPPER 2 (BY SIMILARITY).
COPPER 3 (BY SIMILARITY).
COPPER 4 (BY SIMILARITY).
COPPER 5 (BY SIMILARITY).
COPPER 6 (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
                                                  SUBUNIT: TARANTULA HEMOCYANIN IS A 24-CHAIN POLYMER WITH SEVEN
                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Copper; Glycoprotein; Hemolymph. BY SIMILARITY. BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65.6%; Score 42; DB 1; Length 628; 57.1%; Pred. No. 33; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72017 MW; 539C94849CC8D4F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Virion infectivity factor (SOR protein) (Q protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-AUG-1991 (Rel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 172 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Simian immunodeficiency virus (isolate GB1).
                                                                                                                                                                                                                                                                                                                           InterPro; IPR000896; Hemocyanin,
InterPro; IPR00203; hemocyanin,
InterPro; IPR002203; hemocyanin,
InterPro; IPR002204; Tyrosinase,
Ffam; PF00372; hemocyanin; 1.
Ffam; PF03722; hemocyanin, 2.
Pfam; PF03722; hemocyanin, 2.
PR0SITE; PS00209; HEMOCYANIN 1; 1.
PR0SITE; PS00210; HEMOCYANIN 1; 1.
PR0SITE; PS00210; HEMOCYANIN 2; 1.
PR0SITE; PS00498; TYROSINASE_2; 1.
Transport; Oxygen transport; Copper; INTER MET
INTERPORTED S33 S81 BY SIMIL
                                                                                                                                                                                                                                                                                                   EMBL; AJ277491; CAB89496.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 5/...
A; Conservative
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628 AA;
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P22383;
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TBUJIMOTO H., Hasegawa A., Maki N., Fukasawa M., Miura T., Speidel S., Cooper R.W., Moriyama E.N., Gojobori T., Hayami M.; "Sequence of a novel simian immunodeficiency virus from a wild-caught
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND VARIANTS SER-15; VAL-177 AND ASP-250. Ridder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q., Nickerson D.A.; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proteinase activated receptor 3 precursor (PAR-3) (Thrombin receptor-
like 2) (Coagulation factor II receptor-like 2).
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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J. Biol. Chem. 273:15061-15068(1998).
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Ishihara H., Cornolly A.J., Zeng D., Kahn M.L., Zheng Y.-W.,
Timmons C., Tram T., Coughlin S.R.;
"Proteage-activated receptor 3 is a second thrombin receptor in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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62.5%; Pred. No. 20;
iive 1; Mismatches 2; Indels
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                                                                                                        Nature 341:539-541(1989).
-!- FUNCTION: DETERMINES VIRUS INFECTIVITY.
-!- MISCELLANEOUS: THIS IS AN AFRICAN MANDRILL ISOLATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE 172 AA; 20499 MW; 205E7BDDE6265FCB CRC64;
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15-JUL-1998 (Rel. 36, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M27470; AAB49570.1; -.
InterPro; IPR000475; Viral_infect.
Dam, PP00559; VIf; 1.
PRINTS; PR00349; VIRIONINFECT.
ProDom; PD000063; Viral_infect; 1.
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Les 5; Conservative
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                                                                                                                                                                                                                                                                                                                                  MIM, 601919; ...

GO; GO:0005887; C:integral to plasma membrane; TAS.

GO; GO:0005887; C:integral to plasma membrane; TAS.

GO; GO:001505; P:thrombin receptor activity; TAS.

GO; GO:000756; P:blood coagulation; TAS.

GO; GO:0009611; P:response to wounding; TAS.

GO; GO:0009611; P:response to wounding; TAS.

Enterpro; IPR000276; GPCR_Rhodpsn.

PROSTITE; PS000237; GFCRRHODOPSN.

PROSTITE; PS00237; GFROTEIN RECEP_F1 1; 1.

PROSTITE; PS00237; GFROTEIN RECEP_F1 2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;

Blood coagulation; Polymorphism.
                   CYTOPLASMIC (POTENTIAL).
CLEAVAGE (BY THROMBIN) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
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Kahn M.L., Nakanishi-Matsui M., Shapiro M.J., Ishihara H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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EMBL; AP374726; AAK51564.1; -.
                                                                                                                                                                                                                                                                                                                  Genew; HGNC:3539; F2RL2.
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Voit R., Feldmaier-Fuchs G., Schweikardt T., Decker H., Burmester T.;
"Complete sequence of the 24-mer hemocyanin of the tarantula Eurypelma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Biol. Chem. 275:39339-39344 (2000).
-!- FUNCTION: HEMOCYANINS ARE COPPER-CONTAINING OXYGEN CARRIERS
OCCURRING PREELY DISSOLVED IN THE HEMOLYMPH OF MANY MOLLUSKS AND
                                                                                                                                                                                                                                Gaps
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-!- TISSUS SPECIFICITY: Hemolymph.
-!- TISSUS SPECIFICITY: Hemolymph.
-!- MISCELLANEOUS: THE TWO COPPER LOWS BOUND EACH HAVE 3 NITROGEN LIGANDS (PRESUMABLY CONTRIBUTED BY HIS RESIDUES) AND SHARE A BRIDGING LIGAND (POSSIBLY CONTRIBUTED BY A TYR RESIDUE) IN ADDITION TO BINDING OXYGEN.
-!- SIMILARITY: BELONGS TO THE TYROSINASE FAMILY. HEMOCYANIN
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                                                                                                                                 62.5%; Score 40; DB 1; Length 374;
                                                                                                                                                                                                                                1; Indels
CLEAVAGE.
374 AA; 42508 MW; C45C15A695DD1ABB CRC64;
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1; Mismatches
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Mygalomorphae, Theraphosidae, Aphonopelma.
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InterPro; IPR005203; hemocyanin C.
InterPro; IPR005204; hemocyanin C.
InterPro; IPR00227; Tyrosinase.
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Pfam; PF03723; hemocyanin C; 1.
Pfam; PF03722; hemocyanin N; 1.
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HSSP; P04253; 1LLA.
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nes 5; Conservative
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HCYB_EURCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schartau W., Eyerle F., Reisinger P., Geisert H., Storz H., Linzen B., "Hemcoyanins in spiders, XIX. Complete amino-acid sequence of subunit d from Eurypelma californium hemcoyanin, and comparison to chain e."; Hoppe-Seyler's Z. Physiol. Chem. 364:1383-1409(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Heart;
MEDLINE=20564303; PubMed=10961996;
Voit R., Feldmaier-Fuchs G., Schweikardt T., Decker H., Burmester T.;
"Complete sequence of the 24-mer hemocyanin of the tarantula Eurypelma
                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Biol. Chem. 275:39339-39344 (2000).
-!- FUNCTION: HEMOCYANINS ARE COPPER-CONTAINING OXYGEN CARRIERS OCCURRING FREELY DISSOLVED IN THE HEMOLYMPH OF MANY MOLLUSKS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBLINIT: TARANTULA HEMOCYANIN IS A 24-CHAIN POLYMER WITH SEVEN DIFFERENT CHAINS IDENTIFIED.
-!- SUBCELLULAR LOCATION: Extracellular.
-!- TISSUE SPECIFICITY: Hemolywph.
-!- MISCELLANEOUS: THE TWO COPPER IONS BOUND EACH HAVE 3 NITROGEN LIGANDS (PRESUMABLY CONTRIBUTED BY HIS RESIDUES) AND SHARE A BRIDGING LIGAND (POSSIBLY CONTRIBUTED BY A TYR RESIDUE) IN ADDITION TO BINDING OXYGEN.
-!- SIMILARITY: BELONGS TO THE TYROSINASE FAMILY. HEMOCYANIN
1 (BY SIMILARITY).
1 (BY SIMILARITY).
2 (BY SIMILARITY).
2 (BY SIMILARITY).
2 (BY SIMILARITY).
D (GLCNAC...) (POTENTIAL).
D (GLCNAC...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eurypelma californica (American tarantula).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
                                                                                                                                                                                        ;
                                                                                                                                                       62.5%; Score 40; DB 1; Length 626;
                                                                                                                                                                                        1; Indels
                                                                                                                   17E4FB28C91F9974 CRC64;
                                                                                                                                                                                                                                                                                                                                      HCYD_EURCA STANDARD; PRT; 626 AA. P02241; C9MFH8; 21-0TL-1986 (Rel. 01, Created) 26-0CT-2001 (Rel. 40, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                      64;
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Mygalomorphae; Theraphosidae; Aphonopelma.
NCPI_TaxID=29932;
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InterPro; IPR005203; hemocyanin_C.
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                                                                                                                       71966 MW;
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Nakashima H., Behrens P.Q., Moore M.D., Yokota E., Riggs A.F.; "Structure of hemocyanin II from the horseshoe crab, Limulus polyphemus Sequences of the overlapping peptides, ordering the CNBr Eragments, and the complete amino acid sequence."; J. Biol. Chem. 261:10526-10533(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Limulus polyphemus (Atlantic horseshoe crab).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
Limulidae; Limulus.
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            Pfam; PF00372; hemocyanin; 1.
Pfam; PF0372; hemocyanin; 1.
Pfam; PF03722; hemocyanin; 2; 1.
PFam; PF03722; hemocyanin; 3; 1.
PROSITE; PS00209; HEMOCYANIN; 1.
PROSITE; PS00499; TYROCYANIN; 1.
PROSITE; PS00499; TYROSINASE 2; 1.
Transport; Oxygen transport; Copper; Glycoprotein; Hemolymph.
INIT MET 0 0 COPPER 1 (BY SIMILARITY).
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01-MAR-1989 (Rel. 10, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
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INL -> LN
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[nterPro; IPR005204; hemocyanin_N.
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          InterPro; IPR002227; Tyrosinase.
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  X-RAY CRYSTALLOGRAPHY (2.18 ANGSTROMS).
MEDLINE=93299372; PubMed=8518732;
Hazes B., Magnus K.A., Bonaventura C., Bonaventura J., Dauter Z.,
Kalk K.H., Hol W.G.J.;
"Crystal structure of deoxygenated Limulus polyphemus subunit II
hemocyanin at 2.18-A resolution: clues for a mechanism for allosteric
regulation.";
Protein Sci. 2:597-619(1993).
-!- FUNCTION: HEMOCYANINS ARE COPPER-CONTAINING OXYGEN CARRIERS
OCCURRING FREELY DISSOLVED IN THE HEMOLYMEH OF MANY MOLLUSKS AND
                                                                                                                                                        MEDLINE=91326804; PubMed=1866430; Magnus K.A., Lattman E.E., Volbeda A., Hol W.G.J.; Magnus K.A., Lattman E.E., Volbeda A., Hol W.G.J.; Maxamers of subunit II from Limulus hemocyanin (a 48-mer) have the same quaternary structure as whole Panulirus hemocyanin molecules."; Proteins 9:240-247(1991).
                                                          polyphemus. The amino acid sequence of the largest cyanogen bromide
                   Yokota E., Riggs A.F.; "The structure of the hemocyanin from the horseshoe crab, Limulus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ARTHROPODS.
--- SUBUNIT: HEXAMER OR A WULTIPLE THEREOF.
--- SUBCELLUTAR LOCATION: Extracellular.
--- TISSUE SPECIFICITY: Hemolymph.
--- SIMILARITY: BELONGS TO THE TYROSINASE FAMILY. HEMOCYANIN
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R PDB; ILLA; 20-AUG-94.

R PDB; ILLA; 20-AUG-94.

R PDB; ILLA; 20-AUG-94.

R PDB; ILLA; 20-AUG-94.

R INCEPPO; IPR000896; Hemocyanin.

R InterPro; IPR005203; hemocyanin.

R InterPro; IPR005203; hemocyanin.

R InterPro; IPR005204; hemocyanin.

R InterPro; IPR005204; hemocyanin.

R Pfam; PF0372; hemocyanin.

R Pfam; Pf0087; hemocyanin.

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J. Biol. Chem. 259:4739-4749(1984).
MEDLINE=84185567; PubMed=6715319;
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Best Local Similarity 57.1%; Pred. No. 65;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps
Qy 3 HKWHWYV 9
Db 172 HHWHWL 178
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Search completed: December 16, 2003, 14:15:15 Job time : 5.66667 secs

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Q92521 homo sapien
Q9252 drosophila
Q9bdd drosophila
Q77002 hyphantria
Q9543 drosophila
Q9645 galleria me
Q7651 anopheles
Q811f6 drosophila
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Q94a15 arabidopsis
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027451 bombyx mori
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096533 anopheles g
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MEDLAGE=20098724; PubMed=10631260;

MEDLAGE=20098724; PubMed=10631260;

MEDLAGE=20098724; PubMed=10631260;

MEDLAGE=20098724; PubMed=10631260;

Perez-andor M.A., Abler M.L., Lers A., Green P.J.;

An Hoof A., LeBrasseur N.D., Lers A., Green P.J.;

Tan Hoof A., LeBrasseur N.D., Lers A., Green P.J.;

Tan Stem sensescence in arabidopsis.';

Plant Physiol. 122:169-179 (2000).

REMBL; U90266; AAD00695:1; -.

RESP: PA2289; LAKO.

RICHEPRO; IPR000345; CytC heme bind.

RICHEPRO; IPR003154; SI/Plnuclease.

REMBL; PS02265; Nuclease.

REMBL; PS02190; CYTCCHROWE C; 1.

REMBL; PS00190; CYTCCHROWE C; 1.

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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; camadaulids; Asterales; Asteraceae; Asteroideae;
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Papinutto E., Dundon W.G., Pitulis N., Battistutta R., Montecucco C.,
Zanotti G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97015126; PubMed=8861954; Takahashi M., Inoue N., Ohishi K., Maeda Y., Nakamura N., Endo Y., Fujita T., Takeda J., Kinoshita T.; "Pid-B, a membrane protein of the endoplasmic reticulum with a large lumenal domain, is involved in transferring the third mannose of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Babl; AF374269; AAM18636-1; -.
InterPro; IPR00177; DPS.
InterPro; IPR001519; Ferritin.
                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68.8%; Score 44; DB 2; Length 147; 75.0%; Pred. No. 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GPI anchor.";
BMBO 7. 15:4254-4261(1996),
EMBL; D84436; BAA44827.1; -.
MGD; MGI:1891825; Pigb.
InterPro; IPRO5599; PMP.
Peam; PPO3901; PMP; 1.
SEQUENCE 542 AA; 63133 MW; 0FC3BEBID8A687C1 CRC64;
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PROSITE; PS00818; DPS 1; 1.
SEQUENCE 147 AA; 16649 MW; 2741651884FCCCCD CRC64;
                                                                                                                                          Last sequence update)
Last annotation update)
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Last annotation update)
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                                                          542 AA
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                                                                                                                 Created)
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                                                          PRT;
                                                                                                           01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QRRPQ1;
01-JUN-2002 (TYEMBLYEL 21,
01-JUN-2002 (TYEMBLYEL 21,
01-MAR-2003 (TYEMBLYEL 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00210; ferritin; 1.
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Best Local Similarity 75.vv
6, Conservative
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Best Local Similarity 71.4°
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                                                          PRELIMINARY;
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25 LHNYHWYV 32
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                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
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RESULT 2
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Dolichyl-phosphate-mannose--glycolipid alpha-mannosyltransferase-like
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                                                                                                                                                                                                                                                                                      White O., Bisen J.A., Heidelberg J.F., Hickey B.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D., Ketchum K.A., Nelson K.B., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Kotani
Tabata S., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                            "Genome sequence of the radioresistant bacterium Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68.8%; Score 44; DB 16; Length 159; 62.5%; Pred. No. 21;
                                                                                                                                                                        Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
Deinococcaceae; Deinococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EU Arabidopsis sequencing project;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
BMBL, Al391149; CAC01884.1; ...
InterPro; IRNO5599; PMP.
Pfam; PF03901; PMP; I ransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein; Complete proteome.
SEQUENCE 159 AA; 17309 MW; FB0B9C87ED008F02 CRC64;
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                                                                                   01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) Hypothetical protein DR2142.
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                                  159 AA
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live 2; Mismatches
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Arabidopsis thaliana (Mouse-ear cress).
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01-OCT-2000 (TrEMBLrel. 15, Last seq
01-OCT-2002 (TrEMBLrel. 22, Last anno
                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
                                PRT;
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                                                                                                                                                                                                                                                                        MEDLINE=20036896; PubMed=10567266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE002048; AAF11686.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 286:1571-1577(1999).
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hes 5; Conservative
                                  PRELIMINARY;
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                                                                                                                                                        Deinococcus radiodurans.
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11 VHPWHWWV 18
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                                                                                                                                                                                                          NCBI TaxID=1299;
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                                                                                                                                     DR2142.
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                                    Q9RSI2
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Q9LEQ5
RESULT 4
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68.8%; Score 44; DB 10; Length 498;

Query Match

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306 HPWHWY 311
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                                                                                                                                                                                                                                                                                            3 HKWHWY 8
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  TISSUE=Prostate;
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Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cheuk R., Chen H., Kim C.J., Shinn P., Banh J., Bowser L.,
Cheuk R., Chen H., Kim C.J., Shinn P., Banh J., Bowser L.,
Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,
Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
Tang C.C., Toriumi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S.,
Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AY120693; AAM51236.1; -.
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                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

Koesena B., Chen H., Cheuk R., Kim C.J., Meyers M.C., Shinn P.,

Kabanh J., Bowser L., Carninci P., Dale J.M., Goldsmith A.D.,

Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A.,

Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,

Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,

Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,

Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S.,

Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;

"Arabidopsis cDNA clones.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
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Pfam; PF03901; PMP; 1.
SEQUENCE 548 Aa; 62701 MW; 125D3BEA0BF6A098 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Phosphatidylinositol glycan, class B.
                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) ATSG14850/T9L3_150.
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83.3%; Pred. No. 62;
ive 0; Mismatches
                                                                                                                                                                                                                                                                    (TrEMBLrel. 19, Created)
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nes 5; Conservative
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                          5; Conservative
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                                                                                                            265 HPWHWY 270
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  Best Local Similarity
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SÉOUENCE FROM N.A.
                                                                  3 HKWHWY 8
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01-DEC-2001
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                                                                                                                                                                                                                         Q94A15
Q94A15;
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                          Matches
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Gaps
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MEDLINE=97015126; PubMed=8861954;
Takahashi M., Inoue N., Ohishi K., Maeda Y., Nakamura N., Endo Y.,
Fujita T., Takeda J., Kinoshita T.,
"Pijta T., Takeda J., Kinoshita T.,
"PIG-B, a membrane protein of the endoplasmic reticulum with a large lumenal domain, is involved in transferring the third mannose of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.
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Bukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Bukortera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilade; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68.8%; Score 44; DB 4; Length 554; 83.3%; Pred. No. 69; live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                               Query Match 68.8%; Score 44; DB 4; Length 554; Best Local Similarity 83.3%; Pred. No. 69; Matches 5; Conservative 0; Mismatches 1; Indels
Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; ECO17711; AAH17711.1; -.
Genew; HGNC:8959; PIGB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBO J. 151294-4261(1996).
EMBL; D42138; BAA07709.1; -.
INTERPRO; PRO05599; PMP.
Pfam; PF03901; PMP; 1.
SEQUENCE 554 AA; 65056 MW; BZAF87D13ADF90B3 CRC64;
                                                                                                                                               PFGm; PF03901; PMP; 1.
SEQUENCE 554 AA; 64957 MW; E778418C02A27488 CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAX-2003 (TrEMBLrel. 23, Last annotation update)
CG12006 protein.
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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                                                                                                                           InterPro; IPR005599; PMP.
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Sutton G.C. Workman J.R. Vandell N.D. Zhang O. Chang M. Penderson S.N., and Santon G.C. Workman J.R. Vandell N.D. Zhang O. Chang M. Petitire B.D. Wan K.H. Woole C. Saxere E.G., Helt G., Mollon C.R., Wildon C.R., Barel J. E. Saxere E.G., Helt G., Mollon C.R., Distabled S. S., Mark K.H., Dala A.B. Barel A. Barel J. E. Barelari D. Distabled S. S., Mark R.H., Saxen L. B. Barelari D. Distabled S. S., Mark R.H., Saxen L. B. Barelari D. Distabled S. S., Mark R.H., Saxen L. B. Barelari D. Distabled S. S., Mark R.H., Saxen L. B. Barelari D. Distabled S. S., Mark R.H., Saxen L. S., Distable S. S., Mark R.H., Saxen L. Led Y., Markis B. W. Shirk R.H., Saxen L. S., Mark R.H., Saxen L. S., Mark R.H., Saxen L. S., Mark R.H., Saxen L. S., Shan H., Saxen L. S., Shan R.H., Shan R.H., Mark R.H., Saxen L. S., Shan R.H., Shan R.H., Shan R.H., Shan R.H.,
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Asada N., Hatta T., Norioka S., Kawamoto N.;
"Properties activation and PCR-based sequence of prophenol oxidase A3
in Drosophila melanogaster.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB055857; BAB43866.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hyphantria cunea (Fall webworm).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
                                                                                                                                                                                          Gaps
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01-MAR-2003 (TERBLE-1. 13, Last annotation update)
01-MAR-2003 (TERBLE-1. 23, Last annotation update)
01-MAR-2003 (TERBLE-1. 23, Last annotation update)
00-MAR-2003 (TERBLE-1. 23, Last annotation update)
00X-43 OR DOX-3 OR CG2952.
00X-44 OR DOX-3 OR CG2952.
00X-44 OR DOX-4 OR CG2952.
00X-4 OR CG2952.
00X-
                                                                                                                               68.8%; Score 44; DB 5; Length 561;
83.3%; Pred. No. 70;
ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68.8%; Score 44; DB 5; Length 670; 62.5%; Pred. No. 82; Live 2; Mismatches 1; Indels
FlyBase; FBgn0035464; CG12006.
InterPro; IRR005599; PMP.
Pfam; PF03901; PMP; 1.
SRQUENCE 561 AA; 65006 MW; 5A94054C6E9DB239 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        670 AA.
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InterPro; 1PR005203; hemocyanin_C.
InterPro; 1PR005204; hemocyanin_N.
InterPro; 1PR005227; Tyrosinase.
Pfam; PP00372; hemocyanin; 1.
Pfam; PP00372; hemocyanin; 2.
Pfam; PP03722; hemocyanin; 1.
Pfam; PR00372; hemocyanin; 2.
PROSITE; PR00187; HAEMOCYANIN; 1.
PROSITE; PS00209; HEMOCYANIN; 1.
PROSITE; PS002109; HEMOCYANIN; 1.
PROSITE; PS00210; HEMOCYANIN; 1.
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                                                                                                           Query Match
Best Local Similarity 83.5.
-hea 5; Conservative
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                                                                                                                                                                                                                                                                                                  240 HPWHWY 245
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                                                                                                                                                                                                                                              3 HKWHWY 8
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Q9W1V6
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Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Champe M., Chavez C., Dorsett V., Liao G., Miranda A., Mungall C.J.,
Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
A. Vu C., Lewis S.E., Rubin G.M., Celniker S.;
Labumitted (OCT-2001) to the BMBL/GenBank/DDBJ databases.
BMBL, AYOG1624; AAL29172.1; -.
RENBL, AYOG1624; AAL29172.1; -.
RIVBase; FBGN0000486; Hemocyanin C.
RICEPPO: IPR005203; Hemocyanin C.
RICEPPO: IPR005203; Hemocyanin C.
RICEPPO: IPR005203; Hemocyanin C.
REAM: PF003722; hemocyanin C.
REAM: REAM
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Park D.S., Shin S.W., Kim M.G., Park S.S., Lee W.J., Brey P.T.,
Park H.Y.;
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Bukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 5; Length 683;
84;
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                                                                                                                                                                                                                                                                                                                                                           "Isolation and characterization of the cDNA encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF003723; hemocyanin; 1.
Pfam; PF03723; hemocyanin C: 1.
Pfam; PF03722; hemocyanin N; 1.
PRINTS; PF00187; HEMOCYANIN N; 1.
PROSITE; P5002109; HEMOCYANIN 1; 1.
PROSITE; P500210; HEMOCYANIN 2; 1.
PROSITE; P5004999; TYNOSINASE 2; 1.
SEQUENCE 681 AA; 78195 MW; D85A513318312E83 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                 prophenoloxidase of fall webworm, hyphanitia cunea.";
Insect Biochem. Mol. Biol. 27:983-992(1997).
EMBL; U86875; AAC34251.1; --.
HSSP; P04253; IOXY.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Pred. No.
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InterPro; IPR005203; Hemocyanin C.
InterPro; IPR005204; Hemocyanin N.
InterPro; IPR002277; Tyrosinase.
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62.5%;
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Best Local Similarity 62.3.
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                Arctiidae; Hyphantria.
NCBI_TaxID=39466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             207 LHHWHWHL 214
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Best Local Similarity
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                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SD09866p.
DOX-A3 OR CG2952.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               095R43
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Q95R43
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RX STRAIN-EBREKLEY;

RX Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA George R.A., Lewis S.E., Fineria S. Ashburner M., Henderson S.N.,

Sutton G.G., Roctahan J.R., Yandell M.D., Zhang Q., Chen L.K.,

RA Brandon R.C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Agbayani A., An H.-J., Andraws-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Beans P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Beson K.Y. Benco P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Butler H., Cadieu E., Center A., Chandra I.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davengort L.B., Davies P.,

RA Gloden R., Doup L.E., Downes M., Dugan R., Durbin K.J., Evangeliste C.C., Ferraz C., Ferriera S., Punkov B.C., Dunn P.,

RA Glode A., Gong F., Gorrell J.H., G.Z., Golbart W.M., Glasser K.,

RA Glode A., Gong F., Gorrell J.H., G.Z., Golbart W.M., Glasser R.,

RA Harris N.L., Havery D., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Mouston F., Karlet C., Krarit C., Morris J., Moshrefi A.,

RA Harris N.L., Mauton B. B., WcIntosh T.C., Morris J., Moshrefi A.,

RA Harris N.L., May W. Murphy B., Murphy L., Murny D.M., Nelson D.L.,

RA Harris N.W., Mobarry C., Morris J., Moshrefi A.,

Ra Bazzolo M., Pittuan G.S., Pan S., Pollard J., Worley K., Smith T.,

Ra Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,

Ra Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith H.O.,

RA Harris W. Worse R., Wolson F., Weissenbach J.,

RA Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith H.O.,

RA Sheng Z.Y., Wassarman D.A., Weinsecock G. W. Weissenbach J.,

RA Sheng Z.Y., Wassarman D.A., Weinsecock G. W. Weissenbach J.,

RA Sheng S. R., Roddes E., Subard S., 
                                                                                                                                                                                                                                                                                           Drosophia melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endotterygota; Diptera; Brachycera; Muscomorpha;
Phydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                  683 AA.
                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sem
                                                                                                                                               PRT;
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InterPro; IPR005203; hemocyanin_C.
InterPro; IPR005204; hemocyanin_N.
InterPro; IPR00227; Tyrosinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF03723; hemocyanin_C; 1. PF03722; hemocyanin_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE003459; AAF46946.1; -.
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FlyBase; FBgn0000487; Dox-A3.
                                                                                                                                                      PRELIMINARY;
                                       207 LHHWHWHL 214
2 LHKWHWYV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                             CG2952 protein.
DOX-A3 OR CG2952.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Li D.M., Schmidt O., Theopold U.;
"Insect hemocyte-derived microparticles are regulatory assemblages of the cell-derived immuse response.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF336289; AAK64363.1;
InterPro; IPR005896; Hemocyanin.
InterPro; IPR005203; hemocyanin. C.
InterPro; IPR005203; hemocyanin. N.
InterPro; IPR0052277; Tyrosinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Galleria mellonella (Wax moth).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Pyraloidea;
Pyralidae; Galleriinae; Galleria.
NCBI_TaxID=7137;
                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea, Anopheles.
NCBI_TaxID=7165;
                                                                                                                                                                                                                                                                                                                                                                             0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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                                                                                                                                                                                                                                                                          Query Match 68.8%; Score 44; DB 5; Length 683; Best Local Similarity 62.5%; Pred. No. 84; Matches 5; Conservative 2; Mismatches 1; Indels
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Pfam; PF03722; hemocyanin C; 1.
Pfam; PF03722; hemocyanin N; 1.
PROSTES; PS00209; HEMOCYANIN; N.
PROSTES; PS00210; HEMOCYANIN 1; 1.
PROSTE; PS00210; HEMOCYANIN 2; 1.
PROSITE; PS00498; TYROSTRASE 2; 1.
SRQUENCE 683 AA; 78545 MW; 54AIF80F992839B7 CRC64;
PRINTS; PR00187; HAEMOCYANIN.
PROSITE; PS00209; HEMOCYANIN 1; 1.
PROSITE; PS00210; HEMOCYANIN 2; 1.
PROSITE; PS00498; TYROSINASE 2; 1.
SEQUENCE 683 AA; 79314 MW; 437CBDD9E8A278BF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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Best Local Similarity 62.59
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2964D5
AC Q964D
AC Q964D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. Ahmed A., Lee W.-J., Brey P.T., Ahmed A., Lee W.-J., Brey P.T., "Genomic structure of a prophenoloxidase from the malaria vector,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
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MEDLINE=98119516; PubMed=9459428;
Lee W.J., Ahmed A., della Torre A., Kobayashi A., Ashida M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68.8%; Score 44; DB 5; Length 683; larity 62.5%; Pred. No. 84; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | RMBL; L76038; AAC77383.1; -...
| RMBL; L76038; AAC77383.1; -...
| RSSP; P04255; LOXY. | LOXY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anopheles gambiae.";
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
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Job time : 26 secs
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Les 5; Conserva
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GenCore version 5.1.6
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OM protein - protein search, using sw model

(without alignments)
74.689 Million cell updates/sec December 16, 2003, 14:06:35 ; Search time 5.66667 Seconds Run on:

US-09-870-089B-13

1 KHFKPHGFS 9 BLOSUM62 Scoring table: Title: Perfect score: Sequence:

127863 segs, 47026705 residues Gapop 10.0 , Gapext 0.5 Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	homo	mus m	vign				Q9jvt3 neisseria m		Q98r56 mycoplasma						Q16515 homo sapien							_			Q9fab3 synechocyst	Q9kp73 vibrio chol						CW4	Q27536 caenorhabdi
SUMMERIES	;	D	ATF4 HUMAN	ATF4 MOUSE	PUR7 VIGAC	SAA HORSE	MB11 ARATH	Y4WF RHISN	NAGZ NEIMA	NAGZ_NEIMB	RL34 MYCPU	SODC NEUCR	YBGL ECOLI	RS31 ARATH	RS40 ARATH	VE2 HPV52	BNA1 HUMAN	BNA1 RAT	HS70 PARBR	LSP2 DROME	MCE ASFB7	RL34 STAAM	YCSF BACSU	ACTR_CAVPO	PHOH_ECOLI	YNXO_YEAST	SPKA SYNY3	SYV VIBCH	PA2R BOVIN	POL1 BAYMJ	ABH BACSU	LAMB EMENI		HSF6_ARATH	GAL7 CAREL
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	•	Match Length		349	341	110	642	342	361	361	48	153	244	264	350	368	512	512	649	718	868	45	211	297	354	379	521	953	1463	2410	92	262	289	299	352
940	Query	Match	100.0	89.1	σ	7	67.3	D	S	L()	9	63.6					63.6															٠.	ò	60.0	0.09
		Score	55	49	38	37	37	36	36	36	35	35	35	35	35	35	35	35	35	35	35	34	34	34	34	34	34	34	34	34	33	33	33	33	33
	Result	No.	H	2	m	4	r.	9	7	60	σ,	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

Q39473 cinnamomum Q9hfs2 cochliobolu	P55495 rhizoblum s Q9wxr9 thermotoga	Q92g11 rickettsia P51692 homo sapien	P42232 mus musculu	P52632 rattus norv	Q9tum3 bos taurus	Q9tuz0 sus scrofa	Q13797 homo sapien	Q9h9y6 homo sapien
FATB_CINCA CREA_COCCA	Y41L RHISN UXAC_THEMA	SYGB_RICCN	STSB_MOUSE	STSB_RAT	STSB BOVIN	STSB PIG	ITA9 HUMAN	RPA2 HUMAN
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382	432	670	786	786	787	787	1035	1079
60.0	60.0 60.0	60.0	60.09	0.09	0.09	0.09	0.09	60.0
33	333	33	33.5	33	33	33	33	33
3.4 3.5	36 37	388	40,40	41	42	43	44	45

ALIGNMENTS

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REPUBLINE-20057165; PubMed=10591208;

REPUBLINE-20057165; PubMed=10591208;

REPUBLINE-20057165; PubMed=10591208;

REPUBLINE-20057165; PubMed=10591208;

REPUBLINE-20057165; PubMed=10591208;

REPUBLINE L.J., Ainscound R., Almeida J.P., Babbage A.K.,

REPUBLINE L.J., Barley J., Barlow K.F., Bates K.N., Beasley O.P.,

REPUBLINE L. Button J., Carder C., Carter N.P., Chen Y., Clark G.,

REPUBLINE L. Corby V.E., Cole C.G., Collier R.E., Connor R.,

REPUBLINE L. Corby N.R., Coolile G.J., Cox A.V., Davis J., Dawson E.,

REPUBLINE L., Pey J.M., Fleming K., French L., Garner A.A.,

REPUBLINE L., Hall-Tamlyn G., Heathcott R.W., Ho S., Holmes S.,

REPUBLINE L., Jani-Tamlyn G., Heathcott R.W., Ho S., Holmes S.,

REPUBLINE L., Mall-Tamlyn G., Heathcott R.W., Ho S., Holmes B.J.,

REPUBLINE L., Mall-Tamlyn G., Heathcott R.W., Ho S., Mortimore B.J.,

REPUBLINE L., Mall-Tamlyn G., Heathcott R.W., Ho S., Mortimore B.J.,

REPUBLINE L., Plumb R.W., Ramsey Y., Rogers L., Ross M.T.,

RA Phillips S.H., Plumb R.W., Ramsey Y., Rogers L., Ross M.T.,

RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,

RA Scott C.E., Sehra H.K., Stwee C.D., Smalley M.L., Williet D.L.,

RA Waudin M., Walliams S.A., Williams D.W., Williams L., Williams D.W., Williams L., Williams L., Williams D.W., Williams L., Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=91140735; PubMed=1847461;
Tsujimoto/A., Nyunoya H., Morita T., Sato T., Shimotohno K.;
Tsujimoto/A., Nyunoya H., Morita T., Sato T., Shimotohno K.;
"Isolatioh of cDNAs for DNA-binding proteins which specifically bind to a taxi-responsive enhancer element in the long terminal repeat of human T-fcell leukemia virus type I.";
J. Virol. 65:1420-1426(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLIME=92279218; PubMed=1534408;
Karpjnski BA., Morle G.D., Huggenvik J., Uhler M.D., Leiden J.M.;
Molfcular cloning of human CREB-2: an ATF/CREB transcription factor
that can negatively regulate transcription from the cAMP response
ATEA HUMAN STANDARD; PRT; 351 AA.
P18648; Q9UH31;
P10404-1990 (Rel. 16, Created)
01-NOV-1992 (Rel. 22, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
(5yclic-Amy-dependent transcription factor ATF-4 (Activating transcription factor A) (DNA-biding protein TAXKEB67) (Cyclic AMPresponse element-binding protein 2) (CREB2).
                                                                                                                                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :. Natl. Acad. Sci. U.S.A. 89:4820-4824(1992).
                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEOUENCE FROM N.A.
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STRAIN=CV. Columbia;

XX MEDINE=21016719; PubMed=11130712;

X Theologis A., Ecker J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

XA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

XA White O., Than A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

XA Dunn P., Etgu P., FeldAllyum T.V., Feng J.-D., Forng B., Fulli C.Y.,

XA Dunn P., Etgu P., FeldAllyum T.V., Feng J.-D., Forng B., Fulli C.Y.,

XA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,

XA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin B.,

XI And J. A., Ald S.K., Liu Z.A., Luros J.S., Mariti R., Mariali A.,

XA Hangin-Hooper S., Lie A., Lee J.W., Nierman W.C., Osborne B.I.,

XA Militscher J., Miranda M., Muyen M., Nierman W.C., Osborne B.I.,

XA Pai G., Peterson J., Phan P.K., Rizzo M., Nierman W.C., Osborne B.I.,

Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

XA Mull. Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

XA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

XY Paisar S., Varser C.M., Venter J.C., Davis R.W.;

XY Paisar S., Varser C.M., Venter J.C., Davis R.W.;

XY Paisar S., Varser C.M., Venter J.C., Davis R.W.;

XY Paisar S., Varser C.M., Venter J.C., Davis R.W.;

XY Paisar S., Varser C.M., Venter J.C., Davis R.W.;

XY Paisar S., Varser C.M., Venter J.C., Davis R.W.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Bapermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBL_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                    67.3%; Score 37; DB 1; Length 110;
83.3%; Pred. No. 4.8;
tive 1; Mismatches 0; Indels
                                                                                                                                                      I -> L.
A -> Q.
A -> G.
G -> A.
; BAE7DBE7AB007E5B CRC64;
                                    SMART; SM0197; SAA; 1.

PROSITE; P800992; SAA; 1.

ACULE phase; Plasma; HDL; Amyloid.
CHAIN 1 80 AMYLOID PROTEIN.
CHAIN 1 6 16 1 -> L.

VARIANT 44 44 K -> Q.

VARIANT 59 59 A -> G.

VARIANT 78 78 A -> G.

VARIANT 78 78 A -> G.

VARIANT 78 78 A -> G.

VARIANT 78 A -> G.

SEQUENCE 110 AA; 12289 MW, RABIDBETABOOTESE CRC64.
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-!- SIMILARITY: BELONGS TO THE JACALIN LECTIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Myrosinase binding protein-like Atlg52030
ATIG52030 OR F5F19.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 642 AA.
                    Serum_amyloid_A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AC006216; AAD12677.1; -.
PIR; A95560, A95560.
HSSP; P18674; 1JOT.
InterPro; IPR001229; Jacalin_lectin.
PRINTS; PR00306; SERUMAMYLOID
                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD
                                                                                                                                                                                                                                                                                                                                                                                                                           100 HFRPHG 105
                                                                                                                                                                                                                                                                                                    Local Similarity
es 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                               2 HFKPHG 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                         Query Match
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MB11_ARATH
ID _MB11_A
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                                                                                                              Gaps
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Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-00T-2001 (Rel. 40, Created)
16-00T-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Beta-hexosaminidase (RC 3.2.1.52) (N-acetyl-beta-glucosaminidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Molecular basis of symbiosis between Rhizobium and legumes.";
Nature 387:394-401(1997).
-!- SIMILARITY: TO ALKANAL MONOOXYGENASE ALPHA AND BETA CHAINS
-!- SIMILARITY: TO AGCTERIAL LUCIFERASE). BUT DISTANTLY RELATED.
-!- SIMILARITY: TO Y4VJ.
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InterPro, IRR002103; Bac luciferase.
Fam, PR0021056; Bac Luciferase.
Hypothetical procein; Oxidoreductase; Monooxygenase; Plasmid.
SEQUENCE 342 AA; 37665 MW; EBID57A71EDA89C3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmid sym pNGR234a.
Bacteria, Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae, Rhizobium/Agrobacterium group; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neisseria meningitidis (serogroup A).
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
                                                                        / Match 67.3%; Score 37; DB 1; Length 642; Local Similarity 85.7%; Pred No. 27; Indels ses 6; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h
Similarity 75.0%; Score 36; DB 1; Length 342;
Similarity 75.0%; Pred. No. 22;
6; Conservative 0; Mismatches 2; Indels
6
Pfam; PF01419, Jacalin; 4.
Lectin; Repeat, Miltigene family.
SEQUENCE 642 AA; 68849 MW; 9AB0BS69A6SC913C CRC64,
                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 37.7 kDa protein Y4WF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 361 AA.
                                                                                                                                                                                                                                                                                       PRT; 342 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                            Rhizobium sp. (strain NGR234).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Beta-N-acetylhexosaminidase).
                                                                                                                                                                                                                                                                                       STANDARD;
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                                                                                                                                                                                         157 KHPKPQG 163
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                                                                                                                                                     1 KHFKPHG 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=394;
                                                                                                                                                                                                                                                               F RHISN
Y4WF RHISN
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Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H., Oin H., Vamathevan J., Cotton M.D., Utterback T.R., Khouri H., Oin H., Vamathevan J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.; "Complete genome sequence of Neisseria meningitidis serogroup B strain
                                                                                                                                                                              Science 287:1809-1815(2000).

-!- FUNCTION: Cleaves GlonAc linked beta-1,4 to MurnAc tripeptides

-!- FUNCTION: Cleaves GlonAc linked beta-1,4 to MurnAc tripeptides

(By similarity).

-!- CATALYTIC ACTIVITY: Hydrolysis of terminal non-reducing N-
acetyl-D-haxosamine residues in N-acetyl-beta-D-haxosaminides.

-!- PATHWAY: Call wall synthesis; murcin tripeptide recycling pathway.

-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

-!- SUBCELLULAR: BELONGS TO FAMILY 3 OF GLYCOSYL HYDROLASES. NAGZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Galisson F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmonis.";
Nucleic Acids Res. 29:2145-2153(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -! SIMILARITY: BELONGS TO THE L34P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAMAP; MF_00364; -; 1.
InterPro; IPR01764; Glyco_hydro_3N.
Pfam; PF00933; Glyco_hydro_3; J.
Pfam; PF00975; GLYCOSTL_HYDROL_F3; FALSE_NEG.
Hydrolase; Glycosidase; Peptidoglýcan synthesis; Cell division;
Cell wall; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria, Firmicutes, Mollicutes, Mycoplasmataceae, Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21267165; PubMed=11353084; Chambaud I., Heilig R., Ferris S., Barbe V., Samson D., Gallis Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha B.P.C., Blanchard A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65.5%; Score 36; DB 1; Length 361; 75.0%; Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
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Last annotation update)
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE002408; AAF40960.1; -. PIR; B81190; B81190.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 AA; 39152 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50S ribosomal protein L34. RPMH OR MYPU 1540.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 75.0 ses 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40,
16-OCT-2001 (Rel. 40,
28-FEB-2003 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174 KHFPGHGF 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycoplasma pulmonis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-UAB CTIP
                                                                                                                                                                                                                                                                                                                                                                                            SUBFAMILY
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                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- CATALYTIC ACTIVITY: Hydrolysis of terminal non-reducing N-acetyl-D-hexosamine residues in N-acetyl-beta-D-hexosaminides.
-!- PATHWAY: Call wall synthesis, muran tripeptide recycling pathway.
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SUBCELLULAR: BELONGS TO FAMILY 3 OF GLYCOSYL HYDROLASES: NAGZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=MCS8 / Serogroup B;
MEDLINE=20175755; PubMed=10710307;
Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
                                                                                                                                                                                   Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T., Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S., Jagels K., Leather S., Moule S., Mungall K., Quail M.A., Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J., Mhirehead S., Spratt B.G., Barrell B.G., "Complete DNA sequence of a serogroup A strain of Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                      Nature 404:502-506(2000).
-!- FUNCTION: Cleaves GlonAc linked beta-1,4 to MurNAc tripeptides
(By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last amnotation update)
Beta-hexosaminidase (RC 3.2.1.52) (N-acetyl-beta-glucosaminidase)
                                                                                                            STRAIN=Z2491 / Serogroup A / Serotype 4A;
MEDLINE=20222556; PubMed=10761919;
Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HAMÁD; MF_00364; -; 1.
InterPror IPR001764; Glyco_hydro_3N.
Pfam; PF00933; Glyco_hydro_3; J.
PROSITE; PS00775; GLYCOSYL_HYDROL_F3; FALSE_NEG.
Hydrolase; Glycosidase; Peptidoglýcan synthesis; Cell division;
Cell wall; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neisseria meningitidis (serogroup B).
Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65.5%; Score 36; DB 1; Length 361; 75.0%; Pred. No. 23; 2; Indels tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            174F048B59CAAFBC CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 75.0 les 6; Conservative
                Neisseriaceae; Neisseria.
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                                                                                                                                                                                                                                                                                                                                              meningitidis 22491
                                      NCBI_TaxID=65699;
                                                                                       SEQUENCE FROM N.A
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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J. Biol. Chem. 260:9559-9566(1985).

-!- FUNCTION: Destroys radicals which are normally produced within the cells and which are toxic to biological systems.

-!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = 0(2) + H(2)0(2).

-!- COFACTOR: Binds 1 copper ion and 1 zinc ion per subunit (By
                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=91035418; PubMed=2146266;
Chary P., Hallewell R.A., Natvig D.O.;
Structure, exon pattern, and chromosome mapping of the gene for "Structure, exon pattern, and chromosome mapping of the gene for cytosolic copper-zinc superoxide dismutase (sod-1) from Neurospora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBUNIT: Homodimer.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO THE CU-ZN SUPEROXIDE DISMUTASE FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes, Sordariomycetidae, Sordariales, Sordariaceae, Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lerch K., Schenk E.;
"Primary structure of copper-zinc superoxide dismutase from
                                                                                                                                                                                                                                                                                                                              Score 35; DB 1; Length 48; Pred. No. 4.9;
                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                            MYDULIST: MYDU 1540;
MYDULIST: MYDU 1540;
MYDULIST: MYDU 1540;
INTERPRO 1 PRO00271; Ribosomal L34.
Pram. PRO0468; Ribosomal L34;
Probom, PD003101; Ribosomal L34; I.
IGRFAMS; TIGR01030; rpmH bact; I.
PROSITE; PS00784; RIBOSOMAL L34; I.
Ribosomal Protein; Complete proteome.
SEQUENCE 48 AA; 5581 MW; 72F420BD6EC4DD43 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-APR-1988 (Rel. 07, Created)
01-AUG-1991 (Rel. 19, Dast sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Deproxide dismutase [Cu-Zn] (EC 1.15.1.1).
                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biol. Chem. 265:18961-18967(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=85261356; PubMed=3160699;
                                                                                            EMBL; AL445563; CAC13327.1; -.
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                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 75.0
Matches 6; Conservative
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PIR; A36591; A36591.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97426617; PubMed=9278503; Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99420866; PubMed=10493123;
Fountoulakis M., Takacs M.-F., Berndt P., Langen H., Takacs B.;
"Enrichment of low abundance proteins of Escherichia coli by hydroxyapatite chromatography.";
Electrophoresis 20:2181-2195(1999).
-!- SIMILARITY: STRONG, TO H.INFLUENZAE H11729.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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COPPER AND ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
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Pred. No. 15;
Interpro; IPR001424; SOD_CU_ZN.

PEam; PF001080; Bodcu; 1.

PRINTS; PR00068; CUZNDISMTASE.

PRODOM; P0000469; SOD_CU_ZN; 1.

PROSITE; PS00037; SOD_CU_ZN; 1.

PROSITE; PS00032; SOD_CU_ZN_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
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56DAFAC86CD9573B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                       ZINC (BY SIMILARITY).
COPPER (BY SIMILARITY)
BY SIMILARITY.
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01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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MEDLINE=97061202; PubMed=8905232;
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STRAIN=K12 / MG1655;
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Best Local Similarity
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Salanoubat M., Lemcker, R. Rieger M., Perez-Alonso M., Obernaier B.,
Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
De Simone V., Choisne N., Artiguenave F., Robert C., Brottier P.,
Mincker P., Cattolico L., Weisenbach J., Saurin W., Quetier F.,
Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
Nurmbach E., Drzonek H., Voss H., Holland R., Brandt P., Nyakatura G.,
Wurmbach E., Drzonek H., Voss H., Holland R., Brandt P., Nyakatura G.,
Nyazi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,
Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
Rayarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
RAYARRO R., Laudie M., Berger-Liauro C., Purnelle B., Masuy D.,
A Ge Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
Monfort A., Argintou A., Flores M., Liguori R., Vitale D.,
Monfort A., Argintou A., Flores M., Liguori R., Vitale D.,
Mannaubt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,
                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lopato S., Waigmann E., Barta A.; "Characterization of a novel arginine/serine-rich splicing factor in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P929564; Q944A4; Q9M278;
15-DEC-1998 (Rel. 37, Created)
28-FEB-2003 (Rel. 41, Last aquence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Arginine/serine-rich splicing factor RSP31.
Arginine/serine-rich splicing factor RSP31.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
-!- SIMILARITY: TO B.NIDULANS LACTAM UTILIZATION PROTEIN LAMB AND
                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                             Query Match 63.6%; Score 35; DB 1; Length 244; Best Local Similarity 71.4%; Pred. No. 24; Matches 5; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                   244 AA; 25800 MW; DBC0FD14ADA0EB0A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spermatophyta, Magnoliophyta, eudicotyledons, core eu
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=cv. Columbia;
MEDLINE=21016720; PubMed=11130713;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
MEDLINE=97143875; PubMed=8989882;
                                                                                                                                                                                                EcoGene; EG13308; VbgL.
InterPro; IPR005501; Lamb_YcsF.
Pfam; PF03746; Lamb_YcsF; 1.
Complete protecome.
SEQUENCE 244 AA; 25800 MW· n
                                                                                                                                                           EMBL; AE000174; AAC73807.1; -.
EMBL; D90710; BAA35377.1; -.
PIR; H64806; H64806.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plant Cell 8:2255-2264(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                 B.SUBTILIS YCSF.
                                                                                                                                                                                                                                                                                                                                                                                            101 RHVKPHG 107
                                                                                                                                                                                                                                                                                                                                                             1 KHFKPHG 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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RS31 ARATH
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Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S., Pai G., Militscher J., Sellers P., Gill J.E., Feldblyum T.V., Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C., Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu B., Sasamoto S., Kimura T., Idesawa K., Kawashina K., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakazaki N., Shinpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Tabata S.; Saguence and analysis of chromosome 3 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- SIMILARITY: Contains 2 RNA recognition motif (RRM) domains.
-1- SIMILARITY: BELONGS TO THE SR FAMILY OF SPLICING FACTORS.
-1- CAUTION: Ref.2 sequence differs from that shown due to erroneous gene model prediction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- SUBCELLULAR LOCATION: Nuclear (Potential).
-1- TISSUE SPECIFICITY: Highly expressed in roots and flowers. A presumably longer alternatively spliced form is found in leaves, stems and flowers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=cv. Columbia;
Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
Shinozaki K., Davis B.W., Ecker J.R., Theologis A.;
"RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the SSP consortium (Salk/Stanford/PGEC).";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: REQUIRED FOR CONSTITUTIVE AND ALTERNATIVE PRE-MRNA
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PROSITE; PSG0030; RRM RNP 1; FALSE NEG.
Nuclear protein; RNA-binding; Alternative splicing; Repeat.
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RAA-BINDING (RRM) 2.
ARG/SER-RICH (RS DOMAIN).
R -> K (IN REF. 1).
W; 445FD2E4A5E0C203 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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2; Mismatches
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EMBL; AF439831; AAL27502.1; -.
EMBL; AX125565; AAM78075.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP, P09651, 1HA1.
InterPro; IPR000637; AT hook.
InterPro; IPR000504; RNA_rec_mot.
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                                                                                                                                                                                                                                                                                                                                                                                   Nature 408:820-822(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T51304; T51304.
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A MEDINES FROM NA.

A MEDINES COLUMBIAS,

A MASORGE W., Brandt P., Grivell L.A., Rieger M.,

A MAISORGE W., Brandt P., Grivell L.A., Rieger M.,

A MAISORGE W., Brandt P., Watson M., Schmidthenin T.,

A MAISORGE W., Brandt P., Watson M., Schmidthenin T.,

A MAISORGE W., Brandt P., Watson M., Boultry M., Bencroft I.,

A MAISORGE W., McCullagh B., Blham L., Robben J., Vandenbussche F.,

B Langham S.-A., McCullagh B., Blham L., Robben J., Aundenbussche F.,

B Langham S.-A., McCullagh B., Blham L., Robben J., Aundenbussche F.,

B Langham S.-A., McCullagh B., Blham L., Robben J., Aundenbussche F.,

B Racken M., Wellens I., Vock M., Bastisens I., Aert R., Defoor E.,

B Racken M., Wellens L., Brandster R., Noss M., Hauf J., Korder P.,

B Racken M., Wellen Lankhorst R., Ross M., Hauf J., Korder P.,

B Racken M., Wellen Lankhorst R., Ross M., Hauf J., Korder P.,

B Berneiser S., Hempel S., Feldpausch M., Iamberth S., Van den Daele H.,

B Berneiser S., Hempel S., Feldpausch M., Iamberth S., Van den Daele H.,

B Berneiser S., Hempel S., Feldpausch M., Iamberth S., Wan Bones V.,

B Berneiser S., Hempel S., Feldpausch M., Iamberth S., Wan Bones V.,

B Berneiser S., de Haan M., Mazse A.C., Schaefer M., Macher T.-H.,

B Corkova D., Blocker M., Marzen A.C., Schaefer M., Manner D., Herzl A.,

B Berneiser S., de Haan M., Mazse A.C., Schaefer M., Manner D.,

B Berneiser S., de Haan M., Mazse A.C., Schaefer M., Manner D.,

B Berneiser S., de Haan M., Marzen A.C., Schaefer M., Barques M., Bacher A.,

B Berneiser S., Monicott A., Casaulberta B.,

B Chefdor F., Cooke R., Berger C., Monicott A., Casaulberta B.,

B Reither L., Schwarz S., Scholler P., Heber S., Schee F., Scholler P., Heber S., Scholl M., Marzey D., Schee P., Coordes M., Babermann K.,

B Racker D., Bernel D., Mardis E., Dante M., Abbort M., Schee P., Coorde
                                      Arabidopais thallana (Mouse-ear cress).
Eukaryota; thallana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lopato S., Waigmann E., Barta A.; "Characterization of a novel arginine/serine-rich splicing factor in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRALIE-CV. Columbia,
Wintz H., Askancto M.;
submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                       STRAIN=cv. Columbia;
MEDLINE=97143875; PubMed=8989882;
         RSP40 OR AT4G25500 OR M7J2.130.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plant Cell 8:2255-2264(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Delius H., Hofmann B.;

"Primer-directed sequencing of human papillomavirus types.";

Curr. Top. Microbiol. Immunol. 186:13-31(1994).

-!- FUNCTION: E2 REGULATES VIRAL TRANSCRIPTION AND DNA REPLICATION.

-!- FUNCTION: E2 REGULATES VIRAL TRANSCRIPTION AND DNA REPLICATION.

IT BINDS TO THE EXER RESPONSE ELEMENT (5'-ACCINNININGGT-3') PRESENT

IN MULTIPLE COPIES IN THE REGULATORY REGION. IT CAN ETHER ACTIVATE OR REPRESS TRANSCRIPTION DEPENDING OF EZRE'S POSITION WITH REGARDS TO PROXIMAL PROMOTER ELEMENTS. REPRESSION OCCURS

BY STERICALLY HINDERING THE ASSENBLY OF THE TRANSCRIPTION INITIATION COMPLEX. THE E1-E2 COMPLEX BINDS TO THE ORIGIN OF DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
         -1- FUNCTION: REQUIRED FOR CONSTITUTIVE AND ALTERNATIVE PRE-MRNA SPLICING (BY SIMILARITY).
-1- SUBCELLULAR LOCATION: Nuclear (Potential).
-1- TISSUE SPECIFICITY: Highly expressed in roots and flowers. A presumably longer alternatively spliced form is found in leaves.
                                                                                                                                                   -!- SIMILARITY: Contains 2 RNA recognition motif (RRM) domains.
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0
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DOMAIN 2 74

RNA-BINDING (RRM) 1.

DOMAIN 97 168

RNA-BINDING (RRM) 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 35; DB 1; Length 350;
Pred. No. 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human papillomavirus type 52.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
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K -> R (IN REF. 3).

F -> T (IN REF. 3).

S -> T (IN REF. 3).

4AlC779BB94B32A6 CRC64;
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ARG/SER-RICH (RS DOMAIN).
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01-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
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2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTERPLO; JPR000504; RNA_rec_mot.
Pfam; PF00076; rrm; 2.
SMART; SM00360; RRM; 2.
PROSITE; PS0102; RRM; 2.
PROSITE; PS01030; RRM_RNP_1; FALSE_NEG.
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MEDLINE=94265501; PubMed=8205838;
                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U76607; AAB18813.1; -.
EMBL; AL022197; CAA18176.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h 63.6%;
Similarity 71.4%;
5; Conservative ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
Nature 402:769-777(1999).
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92
350
27
63
66
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                                                                                                                                  stems and flowers.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10618;
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P36796:
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VE2 HPV52
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Job time : 6.66667 secs
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                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   016515; 01353; 01353; 0reated) 01.NOV-1997 (Rel. 35, Created) 01.NOV-1997 (Rel. 35, Last sequence update) 01.NOV-1997 (Rel. 35, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) 03.FEB-2003 (Rel. 41, Last annotation update) 03.FEB-200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryoča, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                            HSSP; P17383; DDHM.

INTERPRO; PR001086; E2_N.

Pfam; PP00511; E2_C; 1.

Pfam; PP00508; E2_N; 1.

ProDom; PD000672; E2_N; 1.

ProDom; PD000678; E2_N; 1.

ProDom; PR000678; E2_N; 1.

ProTom; PR000678; E2_N; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63.6%; Score 35; DB 1; Length 368; 55.6%; Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 512 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
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                       -:- SUBUNIT: Binds DNA as a dimer.
-!- SUBCELLULAR LOCATION: Nuclear.
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MEDLINE=97188490; PubMed=9037075;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=96209957; PubMed=8631835;
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                                                                                                                                                                                                                                                                                 EMBL; X74481; CAA52588.1; -.
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Best Local Similarity 55.v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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                                                                                                                                                                                                                                                                                                             S36576; S36576.
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  REPLICATION
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INTERACTION WITH PRKCABP.

MEDLINE=21661460; PubMed=11802773;

Hruska-Hageman A.M., Wemine J.A., Price M.P., Welsh M.J.;

Kinase I) with the non-voltage gated sodium channels BNC1 (brain Na+channel 1) and ASIC (acid-sensing ion channel).";

Biochem J. 361:443-450(2002).

-I. FUNCTION: Non-voltage-gated amiloride-sensitive cation channel permeable for sodium, potassium and lithium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                    permeable for sodium, potassium and lithium.
--- SUBUNIT: Interacts with PRKCABP.
--- SUBCELLULAR LOCATION: Integral membrane protein.
--- TISSUE SPECIFICITY: BRAIN AND SPINAL CORD.
--- SIMILARITY: BELONGS TO THE AMILORIDE-SENSITIVE SODIUM CHANNEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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7C95B0B32EFF2814 CRC64;
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InterPro; IPR001873; Na+channel ASC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO1078; AMINACHANNEL.
TIGRFAMS; TIGRO0859; ENaC; 1.
PROSITE; PS01206; ASC; 1.
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EMBL; U50352; AAC50432.1; -.
EMBL; U57352; AAB49182.1; -.
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 16, 2003, 14:06:35; Search time 5.6667 Seconds (without alignments)
74.689 Million cell updates/sec

Title: US-09-870-089B-13 Perfect score: 55 Sequence: 1 KHFKPHGFS 9 Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 127863 segs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	P18848 homo sapien	mus n	Q07463 vigna aconi				• •			P07509 neurospora										Q99qtl staphylococ		Q9zls9 cavia porce		P53861 saccharomyc		Q9kp73 vibrio chol				-	2h07	CW4	7536
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Q39473 cinnamomum	Q9hfs2 cochliobolu	P55495 rhizobium s	Q9wxr9 thermotoga	Q92g11 rickettsia	P51692 homo sapien	P42232 mus musculu	P52632 rattus norv	Q9tum3 bos taurus	Q9tuz0 sus scrofa	Q13797 homo sapien	Q9h9y6 homo sapien
FATB_CINCA	CREA COCCA	Y41L RHISN	UXAC THEMA	SYGB_RICCN	STSB_HUMAN	STSB_MOUSE	STSB RAT	STSB_BOVIN	STSB_PIG	ITA9 HUMAN	RPA2_HUMAN
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34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Minoshima S., Kawasaki K., Sasaki T., Makawa S., Rudch J.,

A., Shireni S., Doran D., Song L.,

R. Mana G., Wang Y., Marg G., China Y., Ray L., Ren O., Shahil S., Shoan D., Song L.,

R. Allan M., Shang G., China Y., Ray L., Sen O., Shahil S., Shoan D., Song L.,

R. Allan M., Shang G., China S., Shire J., Willingham D., Wu H., Yao Z.,

R. Allan M., Shang G., China S., Shire J., Willingham D., Wu H., Yao Z.,

R. Cheel J., Lewis S., Shire J., Wang S., Walledhaw H., Shure S.,

R. Cheel J., Shirwan G., China S., Shire J., Walled B., Warescon R., Wilson B.,

R. Cheel J., Shirwa B., Shan M., Landadha H., Shirta S., Badari M., Kadra D.,

R. Cheel J., Shirwa B., Shan M. I., Dumanski J. P., Peyrard W., Kadra D.,

R. Cheel J., Shirwa B., Shan M. I., Dumanski J. P., Shirwa S., Lane L.,

R. Milkinson P., Bodonteck A., Harrman K., Hu X., Khan A.S., Lane L.,

R. Tilahu W. Wight H.,

R. Manaser R.D., Collins S., Wagner L. B., Shemer M. B.,

R. Shirwan M., Sepheroc C. Luna Checkman K., Hu X., Khan A.S., Lane L.,

R. Manaser R.D., Collins S., Magner L. B., Shemen R. D.,

R. Altechul S., Warder B., Buerow K.H., Schwafer C.R., Shan M.,

R. Shanser R.D., Collins S., Magner L. B., Shemen R.D.,

R. Shanser R.D., Collins S., Cacherg B., Buerow K.H., Schwafer C.R., Shule C.R.,

R. Manaser R.D., Collins S., Magner L. B., Derge J.G.,

R. Altechul S., Warshi H.,

R. Robertos S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Bulky S. W.,

R. Robertos S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Bulky S. W.,

R. Robertos S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Bulky S. W.,

R. Robertos S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Bulky S. W.,

R. Robertos S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Bulky S. W.,

R. Robertos S., Worley K.C., Garwood R.J., Wadan A., Sabulu B
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GO; GO:0003677; F:DNA binding activity; TAS.
GO; GO:0003677; F:DNA binding activity; TAS.
GO; GO:0003707; F:DNA bolymerase II transcription factor acti. . .; TAS.
INTERPO; IPRO04827; TF bZIP.
Pfam; PF00170; bZIP; 1.
SMART; SM0038; BRLZ; 1.
PROSITE; PS0036; BZIP BASIC; 1.
TRANSCRIP; PS0036; BZIP BASIC; 1.
TRANSCRIP; PS0036; BZIP BASIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _TTF4_MOUSE STANDARD; PRT; 349 AA.

Q06597; Q61906;
Q1-FBB-1996 (Rel. 33, Created)
Q1-FBB-1996 (Rel. 33, Last sequence update)
Z8-FBB-2003 (Rel. 41, Last annotation update)
Cyclic-AMP-dependent transcription factor ATF-4 (C/EBP-related ATF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUB=Adipocyte;

PUBDLINE=281642; PubMed=8506317;

Vallejo M., For D., Miller C.P., Habener J.F.;

"C/ATF, a member of the activating transcription factor family of DNA-binding proteins, dimerizes with CAATF, enhancer-binding proteins and directs their binding to CAMP response elements."; Proc. Natl. Acad. Sci. U.S.A. 90:4679-4683(1993).
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STRAIN=CD-1; TISSUB=Embryo;
MEDLINE=923351831; PubMed=1631061;
Chevray P.M., Nathans D.;
"Protein interaction cloning in yeast: identification of mammalian proteins that react with the leucine zipper of Jun.";
Proc. Natl. Acad. Sci. U.S.A. 89:5789-5793(1992):
-i- FUNCTION: BINDS TO ASYMMETRIC CAMP RESPONSE ELEMENTS (CRE) AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 55; DB 1; Length 351; 100.0%; Pred. No. 0.0079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /FILGE-VAR. U14.08.

F -> G (IN REF. 3).

T -> R (IN REF. 2).

KEL -> REW (IN REF. 5).

KEL -> LEW (IN REF. 5).

I -> L (IN REF. 5).

W; 7A708C5CCD6ED7F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEUCINE-ZIPPER (PROBÀBLE).
E -> D (in dbSNP:1803324).
/FTId=VAR_014768.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASIC MOTIF.
                                                                         AL022312; CAB45284.1; -. BC008090; AAH08090.1; -. BC011994; AAH11994.1; -. BC024775; AAH24775.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38558 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.08;
                           EMBL; D90209; BAA14234.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C/ATF) (TAXREB67 homolog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9; Conservative
                                                 M86842; AAA52071
                                                                                                                                                                                                                                                                          HGNC: 786; ATF4.
                                                                                                                                                                                             PIR; A45377; A45377.
PDB; 1C16; 04-DEC-00.
TRANSFAC; T01303; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KHFKPHGFS 9
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329 3
338 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
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322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANT
                                                                                                                                                                                                                                                                                   Genew;
                                                    EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
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ATF4_MOUSE
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